

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2004, 18:13:48 ; Search time 13687 Seconds

(without alignments)
 11466.729 Million cell updates/secTitle: US-10-045-072-1
 Perfect score: 3621

Sequence: 1 tggggcggttagatccctg.....tgatcgtcgtttcccaa 3621

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vt:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vt:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rnd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3621	100.0	3621	6	AR123974	Sequence AR123974
2	3621	100.0	3621	6	AR213173	Sequence AR213173
3	3621	100.0	3637	1	AF038548	Corynebac Corynebac
4	3621	100.0	3320	5	AP05276	Corynebac
5	3621	100.0	3499	6	AX127145	Sequence Y09548
6	3578	98.8	3728	1	CGPYC	
7	3578	98.8	3728	6	A97276	Sequence 1 BD140686 Method fo
8	3578	98.8	3728	6	BD140686	Sequence AF503915 Corynebac
9	3469	95.8	3657	1	AF503915	Corynebac
10	3420	94.4	3420	6	AX120849	Sequence BD162966 Novel pol
11	3420	94.4	3420	6	BD162966	Sequence AX453601
12	3398	93.9	3474	6	AX453601	Sequence AX453603
13	3398	93.9	3474	6	AX453603	Sequence AP005216 Corynebac
14	2282	63.0	308750	1	AP005216	Streptomy BD094153 Genes for
15	2279	63.0	4013	6	BD094153	BD094153 Genes for AB083299 Corynebac
16	2279	63.0	4851	1	BX248355	BX248355 Corynebac
17	1927	53.2	341553	1	AE007125	Mycobacte BX248355 Corynebac
18	1708	47.2	1719	6	AX064993	Sequence AX064995 Sequence
19	1395	38.5	1406	6	AX064995	Sequence AL939105 Streptomy AF262949 Mycobacte AF262949 Mycobacte
c	20	1344	37.1	291000	1	SCO939105 MTU0024
c	21	1328	2.2	36.7	42118	1
c	22	1294	4.4	35.7	17992	1
c	23	1294	4.4	35.7	348676	15
c	24	1292	8.8	35.7	318050	1
c	25	1249	6.6	34.5	MTU0024 MSGY2	
c	26	1249	6.6	34.5	31175	1
c	27	1249	6.6	34.5	31176	1
c	28	1033	28.5	1083	6	AR345347 Sequence AX064989 Sequence
c	29	1033	28.5	1083	6	AX064991 Sequence AX064985 Sequence
c	30	907	25.0	939	6	AX064985 Sequence AX064987 Sequence
c	31	907	25.0	939	6	BX251412 Tropherym AE016852 Tropherym
c	32	899	24.8	302938	1	AE016852 Tropherym AE017215 Geobacter
c	33	899	24.8	324227	1	AB086371 Pagrus ma AB086371 Pagrus ma
c	34	741	20.5	303862	1	AY185595 Bos tauru AY185595 Bos tauru
c	35	720	19.9	4010	5	AY225510 Sus scrofa AY225510 Sus scrofa
c	36	714	19.7	3994	4	BX640438 Bordetell BX640438 Bordetell
c	37	707	19.5	3537	4	AF09728 Aspergill AF09728 Aspergill
c	38	705	19.5	347786	1	AF509529 Gallus ga AF509529 Gallus ga
c	39	703	19.4	3916	8	BX640424 Bordetell BX640424 Bordetell
c	40	701	19.4	3559	5	U04641 Human pyruv U04641 Human pyruv
c	41	699	19.3	349146	1	BC011617 Homo sapi BC011617 Homo sapi
c	42	691	19.1	3953	9	L09192 Mus musculu L09192 Mus musculu
c	43	691	19.1	4049	9	HSU30891 Human pyru HSU30891 Human pyru
c	44	690	19.1	4067	10	MUSMPYR MUSMPYR
c	45	690	19.1	3960	9	

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	UNCLASSIFIED	UNKNOWN
AR123974	Sequence 1 from patent US 6171833.	Sequence 1 from patent US 6171833.	AR123974	AR123974	GI:14109335			1 (bases 1 to 3621)	
								Sinskey,A.J., Lessard,P.A. and Willis,L.B.	
								Pyruvate carboxylase from corynebacterium glutamicum	
								Patent: US 6171833-A 109-JAN-2001;	
								JOURNAL Location/Qualifiers	

Pred. No. is the number of results predicted by chance to have a

Db	181	AAGGAATAATTACTCTAGTGTCCACTCACACATCCTCAACGTTCCAGCATTAAAAAG	240	QY	1321	GGCGGAGCTGGGGTTCGTCAGCTCGAGTCAGCTCGTGGGAAATCACCGCACAC	1380
QY	241	ATCTTGGTAGAACCGGGCAATCGGGTCCGTGCTTCCGTGAGCACTCGAAACC	300	Db	1321	GGCGGAGCTGGGGTTCGTCAGCTCGTGGGAAATCACCGCACAC	1380
Db	241	ATCTTGGTAGAACCGGGCAATCGGGTCCGTGCTTCCGTGAGCACTCGAAACC	300	QY	1381	TTRGACTCCATGGTGAATGACCTGGCGTGGTCAACTTGTGCTGCTGCTGCT	1440
QY	301	GTTGCAGCACGGTAGCTATTACCCCGTGAAGATCGGGATCATTCACCGCTCTTT	360	Db	1381	TTGACTCCATGGTGAATGACCTGGCTACATTCACCGCTCTTT	1440
Db	301	GTTGCAGCACGGTAGCTATTACCCCGTGAAGATCGGGATCATTCACCGCTCTTT	360	QY	1441	CGTGACAGGGGGTGGTGGCTACCGTGTGGTCAACCAACATGGTTTC	1500
QY	361	GCTCTGTGAAGCTGGTCCGGCATGGTCAACCGTCAAGCCGTACCTGGACATC	420	Db	1441	CGTGACAGGGGGTGGTGGCTACCGTGTGGTCAACCAACATGGTTTC	1500
Db	361	GCTCTGTGAAGCTGGTCCGGCATGGTACCGTCAAGGGTACCTGGACATC	420	QY	1501	TTGGTGGGGTGGTGGCTACCGTGTGGTCAACCAACATGGTTTC	1560
QY	421	GATGAATTATCGGTGAGCTAAAGTTAAAGCAGATGCCATTACCGGGAC	480	Db	1501	TTGGTGGGGTGGTGGCTACCGTGTGGTCAACCAACATGGTTTC	1560
Db	421	GATGAATTATCGGTGAGCTAAAGTTAAAGCAGATGCCATTACCGGGAC	480	QY	1561	GCGATCACCCGGCACCTCCCTCAGGGTCCACCTGTGATGAGGAGGATCCTG	1620
QY	481	TTCCTGTGAAAATGCCAGCTGCCGGAAAGGTGCTGTTATTACTTTATT	540	Db	1561	GCGATCACCCGGCACCTCCCTCAGGGTCCACCTGTGATGAGGAGGATCCTG	1620
Db	481	TTCCTGTGAAAATGCCAGCTGCCGGAAAGGTGCTGTTATTACTTTATT	540	QY	1621	GATTACTTGGAGATGTGACCTGTGAGCTAACAGCTCAAGGATGTTGCA	1680
QY	541	GGCCCCAACCCCAGAGGTTCTGATCTCACCGGTGATAAGTGTGCGG	600	Db	1621	GATTACTTGGAGATGTGACCTGTGAGCTAACAGCTCAAGGATGTTGCA	1680
Db	541	GGCCCCAACCCCAGAGGTTCTGATCTCACCGGTGATAAGTGTGCGG	600	QY	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATGTTGCACTGCCACTGGGTTCCGTGAC	1740
QY	601	AGAAGGGCTGGTCTGCCAGTTGGGAATCCACCCGAGCAAAACATCGTAGAGATC	660	Db	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATGTTGCACTGCCACTGGGTTCCGTGAC	1740
Db	601	AGAAGGGCTGGTCTGCCAGTTGGGAATCCACCCGAGCAAAACATCGTAGAGATC	660	QY	1741	CGCCTGAGGAGCTGGCCAGCCGGTITGCTCTGTGATCTCCGTGAGGAGGACTG	1800
QY	661	GTTAAAAGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGAGTTGCC	720	Db	1741	CGCCTGAGGAGCTGGCCAGCCGGTITGCTCTGTGATCTCCGTGAGGAGGACTG	1800
Db	661	GTTAAAAGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGAGTTGCC	720	QY	1801	GCAGTTACTGATACACCGACTTCCGGATGCCACACCAAGCTCTTGTGCTGAGCTTGTGCT	1860
QY	721	GGACGGGTATGGCTTGTGCTTCACTTGATGAGCTTCCGCAATTAGCAACAGAGCA	780	Db	1801	GCAGTTACTGATACACCGACTTCCGGATGCCACACCAAGCTCTTGTGCTGAGCTTGTGCT	1860
Db	721	GGACGGGTATGGCTTGTGCTTCACTTGATGAGCTTCCGCAATTAGCAACAGAGCA	780	QY	1861	TCATTGGCACTGAAGGCTGGCCAGGGCTGGGAAAGCTGCTGAGCTTGTGCT	1920
QY	781	TCTCGTGAAGCTGAAGGGCTTTCGGCGATGGCGCGTATATGTCGAACGTGCTGATT	840	Db	1861	TCATTGGCACTGAAGGCTGGCCAGGGCTGGGAAAGCTGCTGAGCTTGTGCT	1920
Db	781	TCTCGTGAAGCTGAAGGGCTTTCGGCGATGGCGCGTATATGTCGAACGTGCTGATT	840	QY	1921	GTGAGGGCTGGGGGGGGGACCTAAGTGTGCGGATGCCACACCGCTGGGAGCTACGATGTCG	1980
QY	841	AACCCCTGCAATTAGAAGTGCAGATCCTGGCGATCACACTGGAGAAGTTGACACCTT	900	Db	1921	GTGAGGGCTGGGGGGGGGACCTAAGTGTGCGGATGCCACACCGCTGGGAGCTACGATGTCG	1980
Db	841	AACCCCTGCAATTAGAAGTGCAGATCCTGGCGATCACACTGGAGAAGTTGACACCTT	900	QY	1981	TGGACAGGGCTGGGGATAACCCGGTACCCAGACTCCGTCAGGAGGATGCCACACCGCTGGGAGCTACGATGTCG	2040
QY	901	TATGAACGTGACTGCTCACTGCCAGCTGGTCAACAAAGTTGTGAAATTGCCAGCA	960	Db	1981	TGGACAGGGCTGGGGATAACCCGGTACCCAGACTCCGTCAGGAGGATGCCACACCGCTGGGAGCTACGATGTCG	2040
Db	901	TATGAACGTGACTGCTCACTGCCAGCTGGTCAACAAAGTTGTGAAATTGCCAGCA	960	QY	2041	CGGGCCGCAACACCGCTGGGATAACCCGGTACCCAGACTCCGTCAGGAGGATGCCACACCGCTGGGAGCTACGATGTCG	2100
QY	961	CAGCATTTGGATCCAGAACCTGGCTATGCCATTGGCGATGCCATTGGCGC	1020	Db	2041	CGGGCCGCAACACCGCTGGGATAACCCGGTACCCAGACTCCGTCAGGAGGATGCCACACCGCTGGGAGCTACGATGTCG	2100
Db	961	CAGCATTTGGATCCAGAACCTGGCTATGCCATTGGCGATGCCATTGGCGC	1020	QY	2101	AAGGAAGCTGCAAGCTGGGCAATCGACGAGCTGGGATCTTCGACGGGTTAACGACGCTC	2160
QY	1021	TCCATTGGTACCCAGGGGGGAAACCGTGTGAAATTCTGGGTGACTGAAAGCT	1080	Db	2101	TCCCAAGATGGCTCCAGCAATCGACGAGCTGGGATCTTCGACGGGTTAACGACGCTC	2160
Db	1021	TCCATTGGTACCCAGGGGGAAACCGTGTGAAATTCTGGGTGACTGAAAGCT	1080	QY	2161	TCCCAAGATGGCTCCAGCAATCGACGAGCTGGGATCTTCGACGGGTTAACGACGCTC	2220
QY	1081	GTCTTCATCGAAATTGAAACCAAGTATCCAGGTGACTGAAAGTGTACCC	1140	Db	2161	TCCCAAGATGGCTCCAGCAATCGACGAGCTGGGATCTTCGACGGGTTAACGACGCTC	2220
Db	1081	GTCTTCATCGAAATTGAAACCAAGTATCCAGGTGACTGAAAGTGTACCC	1140	QY	2221	GCTATGGCTTATTCTGGTGTCTCTGATCCAATGAAAGCTCTACACCTGGATTAC	2280
QY	1141	GAGTTGGACCTGGTAAGGGCAGATGGCTGGCAACCCAGGTGACTGAAAGGAAATTG	1200	Db	2221	GCTATGGCTTATTCTGGTGTCTCTGATCCAATGAAAGCTCTACACCTGGATTAC	2280
Db	1141	GAGTTGGACCTGGTAAGGGCAGATGGCTGGCAACCCAGGTGACTGAAAGGAAATTG	1200	QY	2281	TACCTAAAGATGGCAGGAGATCGTCAAGTGTGGGAGATCTGGCCGTGAA	2340
QY	1201	GCTCTGTGACCCAAAGATAAGTCAAGACGGTAACTGGTCAACCTGGGAACTATCACCGTCACTGGCCGTACCTGGGCTCACCA	1320	Db	2341	ATGGCTGGTCTGGCTTCAGCTGGCCGTGCGGTAACCAAGCTGGTCAACCTGGGCTCACCA	2400
Db	1201	GCTCTGTGACCCAAAGATAAGTCAAGACGGTAACTGGTCAACCTGGGAACTATCACCGTCACTGGCCGTACCTGGGCTCACCA	1320	QY	2341	ATGGCTGGTCTGGCTTCAGCTGGCCGTGCGGTAACCAAGCTGGTCAACCTGGGCTCACCA	2400

2401	TTCGATCTGCCAGTGGCACACCCAGCAACTCGGAACTGGCCAGCTGGCAACCTAC	2460	Db	3481	GCTGGAGATGCAGTCGCAATCATCGAGGCTATGAAGATGGAAACAATCACTGCTTCT	3540
2401	TTCGATCTGCCAGTGGCACACCCAGCAACTCGGAACTGGCCAGCTGGCAACCTAC	2460	Qy	3541	GTTGACGGCAAATCGATCGGTTCTGCTGCAACGGAAAGGTGGCGAC	3600
2461	TTTGCTGGAGCTCAAGCTGGTAGCTGGTGCATTGGGCAACCGTGTGGC	2520	Db	3541	GTTGACGGCAAATCGATCGGTTCTGCTGCAACGGAAAGGTGGCGAC	3600
2461	TTTGCTGGAGCTCAAGCTGGTAGCTGGTGCATTGGGCAACCGTGTGGC	2520	Qy	3601	TIGATCGTGTGTTCTAA	3621
2521	ACCACTCCCAGCCATCCCTGCTGCCATTGTTGCTGCAATTGGCACACCGTGTGGC	2580	Db	3601	TIGATCGTGTGTTCTAA	3621
2521	ACCACTCCCAGCCATCCCTGCTGCCATTGTTGCTGCAATTGGCACACCGTGTGGC	2580	Db	3601	TIGATCGTGTGTTCTAA	3621
		RESULT 3				
		AF038548				
		LOCUS				
		DEFINITION			Corynebacterium glutamicum pyruvate carboxylase (pyc) gene,	
		ACCESSION			complete cds.	
		VERSION			AF038548	
		KEYWORDS			AF038548.1 GI:2708716	
		SOURCE				
		ORGANISM				
					Corynebacterium glutamicum	
					Corynebacterium glutamicum	
					Bacteria; Actinobacteridae; Actinomycetales;	
					Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
		REFERENCE			1 (bases 1 to 3637)	
		AUTHORS			Koffas, M.A., Ramamoorthi, R., Pine, W.A., Sinskey, A.J. and Stephanopoulos, G.	
		TITLE			Sequence of the Corynebacterium glutamicum pyruvate carboxylase gene	
		JOURNAL			Appl. Microbiol. Biotechnol. 50 (3), 346-352 (1998)	
		MEDLINE			99019028	
		PUBMED			9802220	
		REFERENCE			2 (bases 1 to 3637)	
		AUTHORS			Koffas, M.A.G., Ramamoorthi, R., Pine, W.A., Sinskey, A.J. and Stephanopoulos, G.	
		TITLE			Direct Submission	
		JOURNAL			Submitted (14-DEC-1997) Chemical Engineering, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA	
		FEATURES			Location/Qualifiers	
		source			1. .3637	
					/organism="Corynebacterium glutamicum"	
					/mol_type="genomic DNA"	
					/strain="21253"	
					/db_xref="taxon:1718"	
					199. .3621	
					/gene="pyc"	
					199. .3621	
					/product="pyruvate carboxylase"	
					/protein_id="AAB92588.1"	
					/db_xref="GI:2708717"	
					/translation="MSMTTSSTLPFKKILVANRGEIAVRAFRAALETGAATVAIYPR	
					EDRGSFHRSFSAEVIRIGTEGSPVKAYLDIDEIIGAAKVKADAIYPGYCFLENAQL	
					GLTQDKIXTHGAALQCRITTEDPNNGRPDGTGDKSRAVTAAKAGLPVIAESTPSKNIDEIVKSAEG	
					ARECAENGITFIGPTPEVLTDLTGDKSRAVTAAKAGLPVIAESTPSKNIDEIVKSAEG	
					QTYPPIFKAVAGGGGRGMRFVASPDELRLKLAEREEAFGDGAVYVERAVINPQH	
					IETOILGDHTGEVVHLYERDCSLQRRHKVVEIAPAQLDPELDRICADAVKFCSR1	
					GYOGAGTVEFLVDEKGHNHFIEMNPRIOVEMTVEVTEVTDLVKAQMRLAAGATLKEL	
					GLTQDKIXTHGAALQCRITTEDPNNGRPDGTGDKSRAVTAAKAGLPVIAESTPSKNIDEIVKSAEG	
					KLFIDPHLLOAPFADDEOGRILLYADVTVNPKPHGVRPKDVAAPIDKLPNIKDLPL	
					PRGSRDRILKOLGPAAFARDLREODALAFTDTFRDAHQSLLATRVRSAFKTRDTGSL	
					KLTFPELLSVEAVNGGATYDVAMRPLFEDPWDRLDELREAMPNVNQMLLRGRNTVGYTP	
					ELIEDNYAAVNEMLGRPTKVTPSSKVVGDLLAHLYGAGVDPADFAADPOKYDI PDSVI	
					AFLRGELGNPPGGWPEPLRTALEGRSEKAPLTEVEPEEOAHLDADDSSKERRNSLNR	
					LIFLPKPTEEFLEHRRREGNTSALDDREFFYGLVEGRETLIRLPDVTRPLLVRLDAISE	
					DDDKGMRNBNVANVNGOIRPMVRDRSVESVTAEKADSNSKGHVAAPFAGVVTVTVVA	

ORIGIN					
Query	Match	Score	DB	Length	
Qy	Best Local Similarity	100.0%	Pred.	No. 0;	Mismatches 0; Indels 0; Gaps
Matches 3621; Conservative 0;					
Db	1 TGGGGGGGTAGATCCTGGGGTTTATTCAATTCACTTTGGCTTGAAAGTCGTGCAGG	3621			
Db	1 TGGGGGGGTAGATCCTGGGGTTTATTCAATTCACTTTGGCTTGAAAGTCGTGCAGG	3621			
Qy	61 TCAGGGGAGTGTGCCGAAACATTGAGGAAAACAAAAACCGATGTTGATTGGGG	61			
Db	61 TCAGGGGAGTGTGCCGAAACATTGAGGAAAACAAAAACCGATGTTGATTGGGG	61			
Qy	121 AATCGGGGGTTACGATACTAGGACCGAGTGACTGCTATCACCCCTTGGGGTCTCTGTG	121			
Db	121 AATCGGGGGTTACGATACTAGGACCGAGTGACTGCTATCACCCCTTGGGGTCTCTGTG	121			
Qy	181 AAAGGAATAATTACTCTAGTGTGAACTCACACATCTAACGGCTTCCAGCATTCAAAG	181			
Db	181 AAAGGAATAATTACTCTAGTGTGAACTCACACATCTAACGGCTTCCAGCATTCAAAG	181			
Qy	241 ATCTTGGTAGCAAACCGGGGAATCGGGTCCGTGCTTCCGTGCAGCACTCGAAACC	241			
Db	241 ATCTTGGTAGCAAACCGGGGAATCGGGTCCGTGACTCACACATCTAACGGCTTCCAGCATTCAAAG	241			
Qy	301 GGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCCACCGCTCTTT	301			
Db	301 GGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCCACCGCTCTTT	301			
Qy	361 GCTTCTGAAGGCTGTCGGCATTTGGTACCGAAGGGCTCACCAAGGTACCTGGACATC	361			
Db	361 GCTTCTGAAGGCTGTCGGCATTTGGTACCGAAGGGCTCACCAAGGTACCTGGACATC	361			
Qy	421 GATGAAATTATGGTGCAGCTAAAGGTTAAAGCAGATGCCATTACCGGGATACGGC	421			
Db	421 GATGAAATTATGGTGCAGCTAAAGGTTAAAGCAGATGCCATTACCGGGATACGGC	421			
Qy	481 TTCCCTGTCTGAAAATGCCAGGGTTCTTGATCTCACCGGTATAAGTCTCCGGGTAACCGCCGG	481			
Db	481 TTCCCTGTCTGAAAATGCCAGGGTTCTTGATCTCACCGGTATAAGTCTCCGGGTAACCGCCGG	481			
Qy	541 GGCCCAAACCCCAGAGGGTCTTGATCTCACCGGTATAAGTCTCCGGGTAACCGCCGG	541			
Db	541 GGCCCAAACCCCAGAGGGTCTTGATCTCACCGGTATAAGTCTCCGGGTAACCGCCGG	541			
Qy	601 AAGAAGGGCTGCAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTCTGGGTGGCC	601			
Db	601 AAGAAGGGCTGCTGCAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTCTGGGTGGCC	601			
Qy	661 GTTAAAGGGCTGCAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTCTGGGTGGCC	661			
Db	661 GTTAAAGGGCTGCTGCAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTCTGGGTGGCC	661			
Qy	721 GGACGGGGTATGGGTTGCTCACCTGATGAGCTTCGCAAATTAGCAACAGAACCA	721			
Db	721 GGACGGGGTATGGGTTGCTCACCTGATGAGCTTCGCAAATTAGCAACAGAACCA	721			
Qy	781 TCTCGTGAAGGCTGAAGGGTTTGGCGATGGCGGTATATGTCGAACGTGCTGTGATT	781			
Db	781 TCTCGTGAAGGCTGAAGGGTTTGGCGATGGCGGTATATGTCGAACGTGCTGTGATT	781			
Qy	841 AACCCCTCAGCATATTGAAGTGCAGATCCTGGCGATCAGTGCAGATCCTGGGATCACACTGGAGAAGTTGTACACCTT	841			
Db	841 AACCCCTCAGCATATTGAAGTGCAGATCCTGGCGATCAGTGCAGATCCTGGGATCACACTGGAGAAGTTGTACACCTT	841			
Qy	901 TATGAACGTCAGTGACTGCTCACTGAGGCTTGTGAAATTGGCCAGCA	901			
Db	901 TATGAACGTCAGTGCTCACTGAGGCTTGTGAAATTGGCCAGCA	901			
Qy	961 CAGGCAATTGGATCCAGAACCTGCGTGAATCGCATTTGTGGGATGCAGTAAGTTCTGGCGG	961			

QY	2101	AAGGAAGCTGCCAGTCCGGGTGGACATCTTCGACGGCTTAACGACGTC	2160	QY	3 181	CTGGATGATCGTGAATTCTTCTACGGCCTGGTCAAGGCCAGACTTGATCCGCCTG	3 240
Db	2101	AAGGAAGCTGCCAGTCCGGGTGGACATCTTCGACGGCTTAACGACGTC	2160	Db	3 181	CTGGATGATCGTGAATTCTTCTACGGCCTGGTCAAGGCCAGACTTGATCCGCCTG	3 240
QY	2161	TCCCAGATGGTCCAGCAATCGACCGCAGTCTGGAGAACACCCGAGGTG	2220	QY	3 241	CCAGATGTCGCCACCCCACTGCTTGTGGATGCGATCTCTGAGCCAGATAAG	3 300
Db	2161	TCCCAGATGGTCCAGCAATCGACCGCAGTCTGGAGAACACCCGAGGTG	2220	Db	3 241	CCAGATGTCGCCACCCCACTGCTTGTGGATGCGATCTCTGAGCCAGATAAG	3 300
QY	2221	GCTATGGCTTATTCTGGTGAATCTCTGATCCAATGAAAGCTCACCCCTGGATTAC	2280	QY	3 301	GGTATGCAAACTGGTGGCCAAACGTCAACGGCAGATCCGCCAATGGGTGGCTGAC	3 360
Db	2221	GCTATGGCTTATTCTGGTGAATCTCTGATCCAATGAAAGCTCACCCCTGGATTAC	2280	Db	3 301	GGTATGCAAACTGGTGGCCAAACGTCAACGGCAGATCCGCCAATGGGTGGCTGAC	3 360
QY	2281	TACCTAAAGATGGCAAGGGAGATCGTCAAGTCTGGCTCACATCTGGCCATTAAAGAT	2340	QY	3 361	CGCTCCGGTGAATCTGGTGAAGTCTGGTCAACGGCAACGGCAGATTCTCCAAAGGCCAT	3 420
Db	2281	TACCTAAAGATGGCAAGGGAGATCGTCAAGTCTGGCTCACATCTGGCCATTAAAGAT	2340	Db	3 361	CGCTCCGGTGAATCTGGTGAAGTCTGGTCAACGGCAACGGCAGATTCTCCAAAGGCCAT	3 420
QY	2341	ATGGCTGGTCTGCTTGGCCAGGCTGGTAACCAAGTGGTCAACGGCAACTGGCCGTGAA	2400	QY	3 421	GTTGCTGCACCATCGTGGTGTGACTGTTGGTCAACGGTGAAGTCAAGTGGTCAAG	3 480
Db	2341	ATGGCTGGTCTGCTTGGCCAGGCTGGTAACCAAGTGGTCAACGGCAACTGGCCGTGAA	2400	Db	3 421	GTTGCTGCACCATCGTGGTGTGACTGTTGGTCAACGGTGAAGTCAAGTGGTCAAG	3 480
QY	2401	TTGATCTGCCAGTGCACGTGCACTGGGTTGGCAGACTGGCAACCTAC	2460	QY	3 481	GCTGGAGATGCACTGGGCTATGAAGATGGCAACAACTCACTGCTTCT	3 540
Db	2401	TTGATCTGCCAGTGCACGTGCACTGGGTTGGCAGACTGGCAACCTAC	2460	Db	3 481	GCTGGAGATGCACTGGGCTATGAAGATGGCAACAACTCACTGCTTCT	3 540
QY	2461	TTTGCTGAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGTCTGGC	2520	QY	3 541	GTGACGGCAAATAATGATGGTGGCTTCTGGTCAACGAAGGTGGGAC	3 600
Db	2461	TTTGCTGAGCTCAAGCTGGTGCAGATGCTGTTGACGGTGTCTGGC	2520	Db	3 541	GTGACGGCAAATAATGATGGTGGCTTCTGGTCAACGAAGGTGGGAC	3 600
QY	2521	ACCACTCCCAGCCATTCCCTGTGCTGCATTGCTGCAATTGGTGGCAT	2580	QY	3 601	TTGATGTCGTGTTCTCAA	3 621
Db	2521	ACCACTCCCAGCCATTCCCTGTGCTGCATTGCTGCAATTGGTGGCAT	2580	Db	3 601	TTGATGTCGTGTTCTCAA	3 621
QY	2581	ACCGGTTGAGCTGGGCTCAAGTGGTCAACTGGGACTGGCTGAGCTCGAGCCGCTACTGGG	2640	RESULT 4			
Db	2581	ACCGGTTGAGCTGGGCTCAAGTGGTCAACTGGGACTGGCTGAGCTCGAGCCGCTACTGGG	2640	AP005276	332050 bp	DNA	linear BCT 08-AUG-2002
QY	2641	CTGTACCTGCCATTGGTCAACCCGCAACCGGTCTACGCCACGAA	2700	LOCUS	Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section		
Db	2641	CTGTACCTGCCATTGGTCAACCCGCAACCGGTCTACGCCACGAA	2700	DEFINITION	3/10.		
QY	2701	ATCCCAAGGGCAAGTGTCCAACCTGGTCAAGGGCACCCGTGGGAT	2760	ACCESSION	AP005276 BA000036		
Db	2701	ATCCCAAGGGCAAGTGTCCAACCTGGTCAAGGGCACCCGTGGGAT	2760	VERSION	AP005276.1 GI:21323419		
QY	2761	CGTTTCAACTCATCGAGACAATACGGCAACTTGGTCAAGGGCACCCGTGGGAT	2820	KEYWORDS	Corynebacterium glutamicum ATCC 13032		
Db	2761	CGTTTCAACTCATCGAGACAATACGGCAACTTGGTCAAGGGCACCCGTGGGAT	2820	SOURCE	Corynebacterium glutamicum ATCC 13032		
QY	2821	AAGGTACCCCATCCATCGAGACAATACGGCAACTTGGTCAAGGGCACCCGTGGGAT	2880	ORGANISM	Bacteria; Actinobacteridae; Actinomycetales;		
Db	2821	AAGGTACCCCATCCATCGAGACAATACGGCAACTTGGTCAAGGGCACCCGTGGGAT	2880	REFERENCE	Corynebacterineae; Corynebacteriaceae; Corynebacterium.		
QY	2881	GTGGATCAGGAGACTTTGCTGCCATCCACAAAGTAGACATCCAGACTCTGTCTAC	2940	AUTHORS	1 Nakagawa,S.		
Db	2881	GTGGATCAGGAGACTTTGCTGCCATCCACAAAGTAGACATCCAGACTCTGTCTAC	2940	TITLE	Complete genomic sequence of Corynebacterium glutamicum ATCC 13032		
QY	2941	GCGTTCCGGGGGAGCTTGTAACCCCTCCAGGTGGCTGCCACGCCACC	3000	JOURNAL	Unpublished		
Db	2941	GCGTTCCGGGGGAGCTTGTAACCCCTCCAGGTGGCTGCCACGCCACC	3000	REFERENCE	2 (bases 1 to 332050)		
QY	3001	CGCGCACTGGAAAGCCGGCTCGAAGGCCACCTCTGAGGAAGAG	3060	AUTHORS	Nakagawa,S.		
Db	3001	CGCGCACTGGAAAGCCGGCTCGAAGGCCACCTCTGAGGAAGAG	3060	TITLE	Direct Submission		
QY	3061	CAGGGCACCTCGACGGCTGATGGATTCCAGGAACGTCGAATGCCCTCAACGCCCTGCTGG	3120	JOURNAL	Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.		
Db	3061	CAGGGCACCTCGACGGCTGATGGATTCCAGGAACGTCGAATGCCCTCAACGCCCTGCTGG	3120	COMMENT	Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida, Tokyo 194-8533, Japan (E-mail:snakagawa@xanagen.com, Tel:81-44-829-3031, Fax:81-44-813-1651)		
QY	3121	TTCCCCGAAGCCAACCGGAAGAGTCCTCGAGCACCGGCTTGGCAACACCTCTGG	3180	FEATURES	This sequence is conducted by collaboration of Kyowa Hakko Kogyo Co. Ltd. And Kitasato University.		
Db	3121	TTCCCCGAAGCCAACCGGAAGAGTCCTCGAGCACCGGCTTGGCAACACCTCTGG	3180	source	Location/Qualifiers		
QY	3181	CTGGATGATCGTGAATTCTTCTACGGCCTGGTCAAGGCCAGACTTGATCCGCCTG	3 240	1. 332050 /organism="Corynebacterium glutamicum ATCC 13032"			
Db	3181	CTGGATGATCGTGAATTCTTCTACGGCCTGGTCAAGGCCAGACTTGATCCGCCTG	3 240	/mol_type="genomic DNA"			
QY	3241	CCAGATGTCGCCACCCCACTGCTTGTGGATGCGATCTCTGAGCCAGATAAG	3 300	/strain="ATCC 13032"			
Db	3241	CCAGATGTCGCCACCCCACTGCTTGTGGATGCGATCTCTGAGCCAGATAAG	3 300	/db_xref="taxon:196627"			
QY	3301	GGTATGCAAACTGGTGGCCAAACGTCAACGGCAGATCCGCCAATGGGTGGCTGAC	3 360	/note="ATCC 13032"			
Db	3301	GGTATGCAAACTGGTGGCCAAACGTCAACGGCAGATCCGCCAATGGGTGGCTGAC	3 360	/gene="Cg10654"			
QY	3361	CGCTCCGGTGAATCTGGTGAAGTCTGGTCAACGGCAACGGCAGATTCTCCAAAGGCCAT	3 420	/codon_start=1			
Db	3361	CGCTCCGGTGAATCTGGTGAAGTCTGGTCAACGGCAACGGCAGATTCTCCAAAGGCCAT	3 420	/transl_table=11			
QY	3421	GTTGCTGCACCATCGTGGTACTGGTCAACGGCAACTGGTACTGGTCAAGGTCAAG	3 480	/product="Carbon starvation protein CstA"			
Db	3421	GTTGCTGCACCATCGTGGTACTGGTCAACGGCAACTGGTACTGGTCAAGGTCAAG	3 480				
QY	3481	GCTGGAGATGCACTGGCAATCATCGAGGCTATGAAGATGGCAACAACTCACTGCTTCT	3 540				
Db	3481	GCTGGAGATGCACTGGCAATCATCGAGGCTATGAAGATGGCAACAACTCACTGCTTCT	3 540				
QY	3541	GTGACGGCAAATAATGATGGTGGCTTCTGGTCAACGAAGGTGGGAC	3 600				
Db	3541	GTGACGGCAAATAATGATGGTGGCTTCTGGTCAACGAAGGTGGGAC	3 600				
QY	3601	TTGATGTCGTGTTCTCAA	3 621				
Db	3601	TTGATGTCGTGTTCTCAA	3 621				

```

protein"
/protein_id="BAB98047_1"
/db_xref="GI:21323420"
/translation="MKKSPKMSPTARVGLLVEFGVIAAVGWAIAFESRGETINSVWLVL
AAVGSYIIFASFYARLIEYKVVKPKDQRATPAEYVNDGKDYYVPTDRRVLFGHFAAIA
GAGPLVGPVMQAQMGYLPGTLLWILGVIFAGAQDYLVLWVSTRRGRSLGQMVRDE
GTVGGAAGGIALATISIMIIIAVLLAVIAGGWVADTSGVEWFTWSKTTLALLIGYGIMMAILP
RPGRVTEVSIIGVALLLAIVGILFARPEVQMPSVTSFALEGNGPVSFGSLFPF
VNLILLAPRDYLSTMKIGVIGLLAVGILFARPEVQMPSVTSFALEGNGPVSFGSLFPF
LFTIACGALSGFHALLSSGGTPKLVEKESQMRMLGYGGMLMESFVAMMALITAVILD
RHLYFSMNAPLALTGGDPATAEWTNSIGLTGADITPEQLSEAAESVGESTVISRTGG
APTLAFGMSEILSGFIGGAGGMKAFWYHFAIMFEALFILTTVDAGTRVAFMMTDTLGN
VPGIIRRFDPSWTVGNWISTVFUCALWGAIIIMGVTDPLGGINVLFPFLGIANQLLAA
IALALVLUVVKKGLYKWWIIPAVPLAWDLIVTMASWQKIFHSDAIGYWAQNANFR
DAKSQGLTEFGAAKSPEAIDAVIRNTMIQGILSILFAVLVLUVVGAAIAVCIKSIRAR
AAGTPLETTEEPDTESEFFAPTGFLASSRDKEVQAMMDERYPGGAPVSSGGH"
2522 . 2725
/gene="Cg10655"
/CDS
2522 . 2725
/gene="Cg10655"
/codon_start=1
/transl_table=11
/product="Hypothetical protein"
/protein_id="BAB98048_1"
/db_xref="GI:21323421"
/translation="MMALTHALWKIPRAVWWTTELMGDTAYSKYVVLKHEHHPDAPI
PTEREYWRARYADQDANPGARCC"
complement (3092 . 3703)
/gene="Cg10656"
complement (3092 . 3703)
/gene="Cg10656"
/codon_start=1
/transl_table=11
/product="Hypothetical protein"
/protein_id="BAB98049_1"
/db_xref="GI:21323422"
/translation="MSNVINLVLMQAHSTHQVNLNLPSSDATDQILATFSSLCCSQ
NRRNVISWVGVPRSSEERVMEIKLTHRSEAVSKRSPFRGITSWQTNRCPTIGNWPDLC
HRTGRANWSTQHGSCLHRCLIVDDDHFLSVRSNLNVGCNASDLVSQVLLVRELFR
RTVGAHFVWNHGNAVTPSQRTNVAHTNSLKSNVGHCKSCVIL"
3750 . 4706
/gene="Cg10657"
3750 . 4706
/gene="Cg10657"
/codon_start=1
/transl_table=11
/product="Uncharacterized protein involved in propionate
catabolism"
/protein_id="BAB98050_1"
/db_xref="GI:21323423"
/translation="MWNTIYQAIGOALHTTTATROSRKGAISSWKAFAFAPAGKMSIE
AVDRAMRGEGAPSPPIWEGEDGVIAWLLSGLDHIYTIPLAEGEAKRALDTTYKEHSA
EYOSQAPIDLARSMGKEKLAQGLDLRDVDSIVLHTSHHHTHYVIGTSNDPQKFDPDAS
RETLDHSIMYIFAVALEDRAWHHERSYAPERAHRRRETIELWNKISTVEDPEWTRRYHS
VDPAEKAFGARAVITFKDGTVVEDELAVADAHPLGARPFAREQYIQKFRTLAEGVVSE
KEQQDRFLDAAQORTHELEDDLSLENLIEDDADILAKAPVIEGLEF"
4715 . 5629
/gene="Cg10658"
4715 . 5629
/gene="Cg10658"
/codon_start=1
/transl_table=11
/product="PEP phosphonotutase and related enzymes"
/protein_id="BAB98051_1"
/db_xref="GI:21323424"
/translation="MFSSAVAPTERKALRAALAAPEIARMPGAFSPLAARAQIQEAGF
EGVYVSGAWVAADLALPDIGLTTLEVAHRSRQIARVTDLPLVLDADTGFGEPMMSAAR
TVSEBLEDAVGAGCHLLEDQVNPKRCGHLDGKEVVGTDIMVRRIAAVNERDEQFVICA
RTDAAGVEGIDSALERAKAYADAGADMIFTEALYSPADFEKERAAVDIPLLANMTEFG
KTELLPAQOLLEDIGYNAVIYPTLRLIAMGQVEQALGDIANTGIQTDWVDRMQHRSRL
YELLRYNEYNAFDQQVFTYSADSYXKPIF"
5658 . 6809
/gene="Cg10659"
/CDS

```

Page 9

GIRAWTNSRKQSKHSQL
 complement(9878 . 12094)
/gene="Cg10664"
 complement(9878 . 12094)
/gene="Cg10664"
/EC number="1.1.1.42"
/note="TIGR00178:monomer_idh: isocitrate dehydrogenase, NADP-dependent"
/codon_start=1
/transT table=11
/product="Monomeric isocitrate dehydrogenase (NADP+)"
/protein_id="BAB98057.1"
/db_xref="GI:21323430"
*/translation="MAKIIWTRTDEAPLLATYSLKPVVVEAAATAGIEVETRDISI
RILAQFPERLTDQKVGNALAEELGELAKTPPEANIIKLPNISASVPQLKA
YDIPELPDNATTDEEKDILARYNAVKGSAVNPVLREGNSDRRAPIAVKNFVKKFPP*

Query	Match	Score	DB	Length	
Best	Local Similarity	Pred.	No.		
Matches	3621;	Mismatches	0;	Indels	
	Conservative			Gaps	
Y	1 TGGGGCGGGTTAGATCCCTGGGGGTATTCACTTCATTCACTTGGCTTGAAAGTCGTGCAGG	100.0%	3621;	DB 1;	Length 332050;
b	37063 TGGGGCGGGTTAGATCCCTGGGGGTATTCACTTCATTCACTTGGCTTGAAAGTCGTGCAGG	100.0%	0;		
Y	61 TCAGGGCAAGTGTGCCGAAACATTGAGAGGAAACAAAAACCGATGTTGATTGGGG	100.0%	0;		
b	37123 TCAGGGCAAGTGTGCCGAAACATTGAGAGGAAACAAAAACCGATGTTGATTGGGG	100.0%	0;		
Y	121 ATCGGGGGTTACGGATACTAGGACGGCAGTGACTGCTATCACCCCTGGCGGTCTTGTTG	100.0%	0;		
b	37183 ATCGGGGGTTACGGATACTAGGACGGCAGTGACTGCTACACATCTTCAACGCTTCTTGTTG	100.0%	0;		
Y	181 AAAGGAATAATTACTCTAGTGTCACTCACACATCTTCAACGCTTCCAGCATTCAAAGG	100.0%	0;		
b	37243 AAAGGAATAATTACTCTAGTGTCACTCACACATCTTCAACGCTTCCAGCATTCAAAGG	100.0%	0;		
Y	241 ATCTTGGTAGCAACCGGGGAAATCGGGGTCCGGTGAAGATCACCCCTGGCGCTCTGGCT	100.0%	0;		
b	37303 ATCTTGGTAGCAACCGGGGAAATCGGGTCCGGTGAAGATCACCCCTGGCGCTCTGGCT	100.0%	0;		
Y	301 GTGCGAGCCACGGTAGCTATTACCCCCGGTGAAGATCATTCACCGCTCTGGCT	100.0%	0;		
b	37363 GTGCGAGCCACGGTAGCTATTACCCCCGGTGAAGATCATTCACCGCTCTGGCT	100.0%	0;		
Y	361 GCTTCTGAAGCTGTCCGGCATTTGGTACCGAAGGCTCACCAAGTCAAGGGTACCTGGACATC	100.0%	0;		
b	37423 GCTTCTGAAGCTGTCCGGCATTTGGTACCGAAGGCTCACCAAGTCAAGGGTACCTGGACATC	100.0%	0;		
Y	421 GATGAAATTATCGGTGCAAGCTAACAAAAGTTAACGGAGATGCCATTACCGGGATAACGGC	100.0%	0;		
b	37483 GATGAAATTATCGGTGCAAGCTAACAAAAGTTAACGGAGATGCCATTACCGGGATAACGGC	100.0%	0;		
Y	481 TTCCCTGTCTGAATAATGCCAGCTGGCCGAGTTGCCCCGGAGTTGCGGAAACGGCATTACTTTATT	100.0%	0;		
b	37543 TTCCCTGTCTGAATAATGCCAGCTGGCCGAGTTGCGGAAACGGCATTACTTTATT	100.0%	0;		
Y	541 GGCCCCAGGGCTCTGGCATTTGGCGAATCCACCGGTATAACCGCCGGTAACCGCCGGCG	100.0%	0;		
b	37603 GGCCCCAGGGCTCTGGCATTTGGCGAATCCACCGGTATAACCGCCGGTAACCGCCGGCG	100.0%	0;		
Y	601 AGAAGGGCTGGCTCTGGCATTTGGCGAATCCACCGGTATAACCGCCGGTAACCGCCGGCG	100.0%	0;		
b	37663 AGAAGGGCTGGCTCTGGCGAATCCACCGGTATAACCGCCGGTAACCGCCGGCG	100.0%	0;		
Y	661 GTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGGCAGTTGCGGACTTGGCG	100.0%	0;		
b	37723 GTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGGCAGTTGCGGACTTGGCG	100.0%	0;		
Y	721 GGACGGCGGTATGCCGTTTGTGCTTCACCTGATGAGCTTCCGAAATTAGCAACAGAAGCA	100.0%	0;		
b	37783 GGACGGCGGTATGCCGTTTGTGCTTCACCTGATGAGCTTCCGAAATTAGCAACAGAAGCA	100.0%	0;		

Qy	781	TCTCGTGAAAGCTGAAGGGCTTTCGGCATGGGGTATATGTCGAAACGGTGTGATT	840
Db	37843	TCTCGTGAAAGCTGAAGGGCTTTCGGCATGGGGTATATGTCGAAACGGTGTGATT	37902
Qy	841	AACCCTAGCATATTGCAACTGGCATTCCGGATCACACTGGAGAACGGTACACCTT	900
Db	37903	AACCCTAGCATATTGCAACTGGCATTCCGGATCACACTGGAGAACGGTACACCTT	37962
Qy	901	TATGAAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAGTTGTGTAAGT	960
Db	37963	TATGAAACGTGACTGCTCACTGCAGCGTCGTCACCAAAAGTTGTGTAAGT	38022
Qy	961	CAGCATTGGATCCAGAACTGGCATTCGGATGCCAGTAAAGTTCTGCCGC	1020
Db	38023	CAGCATTGGATCCAGAACTGGCATTCGGATGCCAGTAAAGTTCTGCCGC	38082
Qy	1021	TCCATTGGTTACCAAGGGGGAAACCGTTGGAATTCTTGCTGACTGAAAGGGCAACCAC	1080
Db	38083	TCCATTGGTTACCAAGGGGGAAACCGTTGGAATTCTTGCTGACTGAAAGGGCAACCAC	38142
Qy	1081	GTCTTCATCGAAATGAAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAAGTCACC	1140
Db	38143	GTCTTCATCGAAATGAAACCCACGTATCCAGGTTGAGCACACCGTGACTGAAAGTCACC	38202
Qy	1141	GAGGTGGACCTGGTGAAGGGGGAGATGCCGCTTGGCTGGTGGCAACCTTGAAAGGAATTG	1200
Db	38203	GAGGTGGACCTGGTGAAGGGGGAGATGCCGCTTGGCTGGTGGCAACCTTGAAAGGAATTG	38262
Qy	1201	GGTCTGAAACCAAGATAAGATCAAGAACCCACGGTGAGCAGCAGTGCAGTGCCTACCCAGG	1260
Db	38263	GGTCTGAAACCAAGATAAGATCAAGAACCCACGGTGAGCAGCAGTGCAGTGCCTACCCAGG	38322
Qy	1261	GAAGATCCAACAAACGGCTTCCGGGAGATACCGGAACTATCACCGGCTCACCA	1320
Db	38323	GAAGATCCAACAAACGGCTTCCGGGAGATACCGGAACTATCACCGGCTCACCA	38382
Qy	1321	GCCCCGAGCTGGGTTCGTCTTGACGGTGAGCTCAGCTCAGCTGGGAAATCACCGCACAC	1380
Db	38383	GCCCCGAGCTGGGTTCGTCTTGACGGTGAGCTCAGCTGGGAAATCACCGCACAC	38442
Qy	1381	TTTGACTCCATGCTGGTGAATAATGACCTGCCGGTCCGACTTGAAACTTGCTGGTGTGCT	1440
Db	38443	TTTGACTCCATGCTGGTGAATAATGACCTGCCGGTCCGACTTGAAACTTGCTGGTGTGCT	38502
Qy	1441	CGTGCACAGGGCGTTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATGGTTTC	1500
Db	38503	CGTGCACAGGGCGTTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATGGTTTC	38562
Qy	1501	TTGGGTGCTGGGAAAGAGGAACTCACTTCCAAGGGCATGCCACGGATTCATT	1560
Db	38563	TTGGGTGCTGGGAAAGAGGAACTCACTTCCAAGGGCATGCCACGGATTCATT	38622
Qy	1561	GCCGATCACCGCACCTCCTTCAAGGTGCTGATGAGCAGGGACGCATCCTG	1620
Db	38623	GCCGATCACCGCACCTCCTTCAAGGTGCTGATGAGCAGGGACGCATCCTG	38682
Qy	1621	GATTACTTGGCAGATGTCACCGTGAACAAGGATCTGCCACGGTCCAAAGGATGGTGC	1680
Db	38683	GATTACTTGGCAGATGTCACCGTGAACAAGGATCTGCCACGGTCCAAAGGATGGTGC	38802
Qy	1681	GGCTCCTATCGATAAGCTGCCCTAACATCAAGGATCTGCCACGGTCTGGTGC	1740
Db	38743	GGCTCCTATCGATAAGCTGCCCTAACATCAAGGATCTGCCACGGTCTGGTGC	38862
Qy	1741	GGCTGAAAGCAGCTGGCCCAGCCGGATGCCACCCAGTCTCGTGCATCTCGTGC	1800
Db	38803	GGCTGAAAGCAGCTGGCCCAGCCGGATGCCACCCAGTCTCGTGCATCTCGTGC	38862
Qy	1801	GCAGTTACTGATAACCACCTTCCGGATGCCACCCAGTCTCGTGCATCTCGTGC	1860
Db	38863	GCAGTTACTGATAACCACCTTCCGGATGCCACCCAGTCTCGTGCATCTCGTGC	38922
Qy	1861	TCATTGGCAACTGAAGCCCTGGGGAGGGGGAGGGCTGCCAAAGGCTGACTCCTGAG	1920

Db	38923	TCAATTGGCACTGAAGCTGCGGAGGGCGGACTACATGTGGCGATGGCTTCTGAGGTTTGTC	38982		Db	40003	GGGTCTCTGGGGAGCTGGTAACCCCTCCAGTGGCTGGCAAGGCCACTGGCACCC 4 0062
Qy	1921	GTGGAGGCCTGGGGGGGGGAAAGCTACATGTGGCGATGGCTTCTTGGGATCCG 1980			Qy	3001	CGCGCACTGGAAAGGCCACTCTGACCGGAAGTTCTGTGAGGAAGAG 3 060
Db	38983	GTGGAGGCCTGGGGGGGAAAGCTACATGTGGCGATGGCTTCTTGGGATCCG 39042			Db	40063	CGCGCACTGGAAAGGCCACTCTGACCGGAAGAG 4 0122
Qy	1981	TGGGACACGGCTCGACAGAGCTGGGGAGATGCCGAATGTAACATTCAAGATGCTGCTT 2040			Qy	3061	CAGGGCACCCTGAGCTGATGATTCCAGGAAACTGTGCAATTAGCCTAACCGCTGCTG 3 120
Db	39043	TGGGACACGGCTCGACAGAGCTGGGGAGATGCCGAATGTAACATTCAAGATGCTGCTT 39102			Db	40123	CAGGGCACCCTGAGCTGATGATTCCAGGAAACTGTGCAATTAGCCTAACCGCTGCTG 4 0182
Qy	2041	GCCCCCGCAACCGTGGGATAACCCCGTACCCAGACTCCGTCTGCGGCTTAACGACGTC 2100			Qy	3121	TTCCCGAAGCCAACCGGAAGAGTTCCCTGAGGCCACTGTGCGCAACACCTCTGCG 3 180
Db	39103	GCCCCCGCAACCGTGGGATAACCCCGTACCCAGACTCCGTCTGCGGCTTGTGTT 39162			Db	40183	TTCCCGAAGCCAACCGGAAGAGTTCCCTGAGGCCACTGTGCGCAACACCTCTGCG 4 0242
Qy	2101	AAGGAAGGTGCCAGCTCCGGGACATCTCCGGCATCTTGACCGGCTTAACGACGTC 2160			Qy	3181	CTGGATCTGTGAATTCTACTGGGCTGGTGAAGGCCGGAGACTTGTATCCGCTG 3 240
Db	39163	AAGGAAGGTGCCAGCTCCGGGACATCTCCGGCATCTTGACCGGCTTGTGAGGTG 39222			Db	40243	CTGGATCTGTGAATTCTACTGGGCTGGTGAAGGCCGGAGACTTGTATCCGCTG 4 0302
Qy	2221	GCTATGGCTTATTCTGGTGTATCTCTGATCCAATGAAAAGCTACACCCCTGGATTAC 2280			Qy	3241	CCAGATGTGGGACCCCACGTGCTGGATGCCAGACGATAAG 3 300
Db	39223	GCTATGGCTTATTCTGGTGTATCCAATGAAAAGCTACACCCCTGGATTAC 39282			Db	40303	CCAGATGTGGGACCCCACGTGCTGGATGCCAGACGATAAG 4 0362
Qy	2281	TACCTAAAGATGGCAGAGGAGATGTCAAGTCTGGGCTCACATCTGGCCATTAGGAT 2340			Qy	3301	GGTAGGGCAATGTGTGGCAACCGCAAGATCCGCCAATGCCAACAGGCCAT 3 360
Db	39343	TACCTAAAGATGGCAGAGGAGATGTCAAGTCTGGGCTCACATCTGGCCATTAGGAT 39342			Db	40423	GGTAGGGCAATGTGTGGCAACCGCAAGATCCGCCAATGCCAACAGGCCAT 4 0422
Qy	2341	ATGGCTGGCTGGCTGGCCAGTGGTAACCAAGTGGTCAACATCTGGCCATTAGGAT 2340			Qy	3421	GTTGCTGCCACCATTCGCTGACCTGTGCTGAAAGGTGATGAGGTCAAG 3 480
Db	39403	ATGGCTGGCTGGCTGGCTGGTAACCAAGTGGTCAACCCGCAACTGGCCACTAC 39462			Db	40483	GTTGAGATGGCACTGGCTGCAATTGAGGTGATGAGGTCAAG 4 0542
Qy	2401	TTCGATCTGCCAGTGCAGTGCAACCCAGACACTGGGGTGGCAGCTGGCAACCTAC 2460			Qy	3481	GCTGGAGATGGCACTGGCTGCAATTGAGGTGATGAGGTCAAG 4 0542
Db	39463	TTCGATCTGCCAGTGCAGTGCAACCCAGACACTGGGGTGGCAGCTGGCAACCTAC 39522			Db	40543	GCTGGAGATGGCACTGGCTGCAATTGAGGTGATGAGGTCAAG 4 0602
Qy	2461	TTTGGCTGAGCTCAAGTGGTGAAGTGGTGTGCTGCCATTGGGCTGGCACCACGTCTGGC 2520			Qy	3541	GTTGACGGCAAATGATGCTGGCTTCTGTGAAAGGAAACAAATCACTGCTTCT 3 540
Db	39523	TTTGGCTGAGCTCAAGTGGTGAAGTGGTGTGCTGCCATTGGGCTGGCACCACGTCTGGC 39582			Db	40603	GTTGACGGCAAATGATGCTGGCTTCTGTGAAAGGAAACAAATCACTGCTTCT 4 0662
Qy	2521	ACCACCTCCAGCCATTCCCTGTGCAACCCGGCACACCCGTGGCATTGGCTGGC 2580			Qy	3601	TTGATCTGTGTTCTCAA 3 621
Db	39583	ACCACCTCCAGCCATTCCCTGTGCAACCCGGCACACCCGTGGCATTGGCTGGC 39642			Db	40663	TTGATCTGTGTTCTCAA 4 0683
Qy	2581	ACCGGTTGAGGCTCGAGGCTGTCTGACCTCGAGGCAAGCTGGACTGGGGGA 2640		RESULT 5			
Db	39643	ACCGGTTGAGGCTCGAGGCTGTCTGACCTCGAGGCAAGCTGGGGGA 39702		AX127145	349980 bp	DNA	PAT 11-MAY-2001
Qy	2641	CTGTACCTGCCATTGAGTCTGGAAACCCAGGGCCAAACCGGTCTACGCCACGAA 2700		LOCUS	from Patent EP1108790.		
Db	39703	CTGTACCTGCCATTGAGTCTGGAAACCCAGGGCCAAACCGGTCTACGCCACGAA 39762		DEFINITION	Sequence 7061		
Qy	2701	ATCCAGGGGACAGTTGTCACAGGCAACCTGGTGCACAGGCCACTGGCCTGGGAT 2760		ACCESSION	AX127145 AX114121		
Db	39763	ATCCAGGGACAGTTGTCACAGGCAACCCAGGGCCAAACCGGTCTACGCCACGAA 39822		VERSION	AX127145.1 GI:14041133		
Qy	2761	CGTTTCGAACCTGAGACAACCTGGTGCACAGGCCACTGGCCTGGGAT 2820		KEYWORDS			
Db	39823	CGTTTCGAACCTGAGACAACCTGGTGCACAGGCCACTGGCCTGGGAT 39882		SOURCE	Corynebacterium glutamicum		
Qy	2821	AAGGTCAACCCATCCCTCAAGGTGGGGACCTCCACCTGGCAACTGGGGGT 2880		ORGANISM	Bacteria; Actinobacteridae; Actinomycetales;		
Db	39883	AAGGTCAACCCATCCCTCAAGGTGGGGACCTCCACCTGGCAACTGGGGGT 39942		AUTHORS	Naikagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.		
Qy	2881	GTGGATCCAGGAGACTTTGCTGGCGATCCAAAAGTAGACATCCAGACTCTGTCA 2940		TITLE	Novel polynucleotides		
Db	39943	GTGGATCCAGGAGACTTTGCTGGCGATCCAAAAGTAGACATCCAGACTCTGTCA 40002		JOURNAL	Patent: EP 1108790-A 7061 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP)		
Qy	2941	GGGTCTCTGGGGAGCTGGTGGTAACCCCTCCAGGTGGCCAGGGCAACTGGCAC 3000		FEATURES	Location/Qualifiers		
Db			Source	1. :349980			
Qy				/organism="Corynebacterium glutamicum"			
Db				/mol_type="genomic DNA"			
Qy				/db_xref="taxon:1718"			
Db				/note="Seq 1 to long_(3.309.400) split in 11, seq 7061 0.600.001 0.949.980 ,"			
Qy				ORIGIN			

Db	107113	AGGAAGGCTCCAGTCCGGACATCTCCGCATCTTGACGGCTTAACGACGT	107172	Qy	3241	CCAGATGTCGCCACCCACTGCTTGGCTGGATGCGATCTTGAGCCAGCATAAG	3300
Qy	2161	TCCAGATGCGTCCAGCAATGACGGAGTCCGGTAGCCGGT 2220		Db	108253	CCAGATGTCGCCACCCACTGCTTGGCTGGATGCGATCTTGAGCCAGCATAAG	108312
Db	107173	TCCAGATGCGTCCAGCAATGACGGAGTCCGGTAGCCGGT 107232		Qy	3301	GGTATGCGAATGTTGGCCAAACGTOAACGGCCAGATCCGCAATGCGTGTGAC	3360
Qy	2221	GCTATGGCTTATTCTGGTGAATCTCTCTGATCAATGAAAGCTCACCCCTGGATTAC	2280	Db	108313	GGTATGCGAATGTTGGCCAAACGTOAACGGCCAGATCCGCAATGCGTGTGAC	108372
Db	107233	GCTATGGCTTATTCTGGTGAATCTCTCTGATCAATGAAAGCTCACCCCTGGATTAC	107292	Qy	3361	CGCTCGTTGAGTCTGTCACCGCAACGGAGATCTCCAAACAAGGCCAT	3420
Qy	2281	TACCTAAAGATGGCAGAGGATCGTCAAGTCTGGCCTAACATCTGGCCATTAAAGGAT	2340	Db	108373	CGCTCGTTGAGTCTGTCACCGCAACGGAGATCTCCAAACAAGGCCAT	108432
Db	107293	TACCTAAAGATGGCAGAGGATCGTCAAGTCTGGCCTAACATCTGGCCATTAAAGGAT	107352	Qy	3421	GTTGCTGCACCATTCGCTGCTGCTGACTGTTGGCTGAAGGTGATGAGGTCAAG	3480
Db	107353	ATGGCTGGTCTGCTGCCAGGTGGTAACCAAGGTTGGTCAACCGCACTGGCTGAA	2400	Db	108433	GTTGCTGCACCATTCGCTGCTGACTGTTGGCTGAAGGTGATGAGGTCAAG	108492
Qy	2341	ATGGCTGGTCTGCTGCCAGGTGGTAACCAAGGTTGGTCAACCGCACTGGCTGAA	107412	Qy	3481	GCTGAGATGCGACCATTCGAGGCTATGAAGATGGAAACAATCACTGCTTCT	3540
Qy	2401	TTCGATCTGCCAGTGCACGGTGGCACCCACGACACTGGGGAGCTGGCAACCTAC	2460	Db	108493	GCTGAGATGCGACCATTCGAGGCTATGAAGATGGAAACAATCACTGCTTCT	108552
Db	107413	TTCGATCTGCCAGTGCACGGTGGCACCCACGACACTGGGGAGCTGGCAACCTAC	107472	Qy	3541	GTTGACGGCAAAATGGATCGCTGCTGCAACGGAAAGGTGAAAGGGTGGCGAC	3600
Qy	2461	TTTGCCTGCAAGCTCAAGCTGGTGAATGCTGGTGAACGGCAACTGTCITGGC	2520	Db	108553	GTTGACGGAAAATGATCGCTGCTGCTGTTGGTGAAGGGTGGAAAGGGTGGCGAC	108612
Db	107473	TTTGCCTGCAAGCTGGTCAAGCTGGTGAATGCTGGTGAACGGCAACTGTCITGGC	107532	Qy	3601	TGATCGTCTGCTGCTTCTCAA 3621	
Qy	2521	ACCACCTCCAGCCATCCCTGTCGCCATTGGTGTGCAATTGGTGTGCAATTGGTGTGCGAT	2580	Db	108613	TGATCGTCTGCTGCTTCTCAA 108633	
Db	107533	ACCACCTCCAGCCATCCCTGTCGCCATTGGTGTGCAATTGGTGTGCGAT	107592				
Qy	2581	ACGGTTTGAAGCTCGAGGCTGAGCTTGACCTCGAGCCGTACTGGAAAGCAGTGGCGGA	2640			RESULT 6	
Db	107593	ACGGTTTGAAGCTCGAGCTTGACCTCGAGCCGTACTGGAAAGCAGTGGCGGA	107652			CGPYC	3728 bp DNA linear
Qy	2641	CTGTACCTGCCATTGAGTCTGGCTGAGCTGGCTTACGCCACGAA	2700			LOCUS	Corynebacterium glutamicum pyc gene.
Db	107653	CTGTACCTGCCATTGAGTCTGGACCCAGGCCAACGGTCTACGCCACGAA	107712			DEFINITION	
Qy	2701	ATCCCAGGGACAGTTGTCACCTGGTCAACGGCACCCACTGGCCTGGGAT	2760			ACCESSION	Y09548
Db	107713	ATCCCAGGGACAGTTGTCACCTGGTCAACGGCACCCACTGGCCTGGGAT	107772			VERSION	Y09548.1 GI:2879822
Qy	2761	CGTTTCAACTCATCGAGACAACGTTGTCGCGATCCACAAAGTCAACC	2820			KEYWORDS	pyc gene; pyruvate carboxylase.
Db	107773	CGTTTCAACTCATCGAGACAACGTTGTCGCGATCCACAAAGTCAACC	107832			ORGANISM	Corynebacterium glutamicum
Qy	2821	AAGGTCAACCCATCCTCCAAGGTGGGACCTCCACACTGGCCTGGGGT	2880			REFERENCE	Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Db	107833	AAGGTCAACCCATCCTCCAAGGTGGGACCTCCACACTGGCCTGGGGT	107892			AUTHORS	Peters-Wendisch, P.G., Kreutzer, C., Kalinowski, J., Patek, M., Sahn, H. and Eikmanns, B.J.
Qy	2881	GTGGATCAGGAGACTTTGTCGCGATCCACAAAGTCAACCTGGGGT	2940			TITLE	Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene
Db	107893	GTGGATCAGGAGACTTTGTCGCGATCCACAAAGTCAACCTGGGGT	107952			JOURNAL	Microbiology (Reading, Engl.) 144 (Pt 4), 915-927 (1998)
Qy	2941	GGCTTCTGGCGGGAGGCTTGGTAACCTCCAGCTGGCAGAGCCACTGGCACC	3000			MEDLINE	98240228
Db	107953	GGTTCTGGCGGGAGGCTTGGTAACCTCCAGCTGGCAGAGCCACTGGCACC	108012			PUBMED	9579065
Qy	3001	CGGCCACTGGAAAGCCGCTCCGAAGGAACCTCTGACGGAAAGTCTGGCAAC	3060			REFERENCE	2 (bases 1 to 3728)
Db	108013	CGGCCACTGGAAAGCCGCTCCGAAGGAACCTCTGACGGAAAGTCTGGCAAC	108072			AUTHORS	Peters-Wendisch, P.G.
Qy	3061	CAGGGCGAACCTGACCCGTGATGATTCCAAGGAACGTGCAATAAGCTCAACCGCTG	3120			TITLE	Direct Submission
Db	108073	CAGGGCGAACCTGACCCGTGATGATTCCAAGGAACGTGCAATAAGCTCAACCGCTG	108132			JOURNAL	Submitted (21-NOV-1996) P.G. Peters-Wendisch, Institut fuer Biotechnologie 1, Forschungszentrum Juelich GmbH, Juelich, D-52425, FRG
Qy	3121	TTCGGAAAGCCAACGGCAACGGTCTCTGAGCTGGCTTCTGGCAACACTCTGG	3180			FEATURES	Location/Qualifiers
Db	108133	TTCGGAAAGCCAACGGCAACGGTCTCTGAGCTGGCTTCTGGCAACACTCTGG	108192			source	1. .3728
Qy	3181	CTGGATGATCGTGAATTCTCTGAGCTGGCTGGCTGAAGGCCCTGATCCGCTG	3240			/organism="Corynebacterium glutamicum"	/organism="Corynebacterium glutamicum"
Db	108193	CTGGATGATCGTGAATTCTCTGAGCTGGCTGGCTGAAGGCCCTGATCCGCTG	108252			/mol_type="genomic DNA"	/mol_type="genomic DNA"

/db_xref="GI:2879823"
/db_xref="GOA:054587"
/db_xref="SPTREMBL:054587"
/translation="MSTHTSSSTLPAPFKKILVANRGEIAVRAFFRAALETGAATVAIYPR
EDRGSSFRSEASEAVRIGTEGSPVKAYLDIDEIIIGAAKKVKADAIYPGYGFLSENAQL
ARECAENGITFIGPTPEVLDLTGDKSRVATAKKAGLPVLAESTPSKNIDEIVKSAG
QTYPIFVKAVAGGGGGGMRFTVASPDELRLKATEASREAAAFCDGAVVERAVINPOH
IEVQILGDHTGEVHLYERDCSLQRHRQKVTEIAPAQHLDPELDRICADAULKFCRSI
GYQGAGTVEFLVDEKGHNHFIEMNPRIQVEHTVTTEEVTVEVDLVKAQMRLAAGATLKL
GLTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAALQCGEIT
AHFDISMLVKMTCRGSDDEFETAVARAQRLADEFTVSGVATNIGFLRALLREEDFTSKRIA
TGFIAJDHPHILLQAPPADDEQQGRILDYLLADVTVNKPHGVRPKDVAAPIDKLPNINIQLPL
PRGSRDRLKQLGPAAFAFDLREQDALAVTDTFRDAHQSSLATRVRSFALKPAAEAVA
KITPELLSVBAWGCGATYDVAMRFLFEDPWDRDLDELREAMPNVNIQMLLRGRNTVGYTP
YPDSSVCRAFVREAASSGVDFRIFDALNDVSQMRPAJDAVLETTNTAVAEVAMAYSGDL
SDPNEKLYTDYLLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVTALARREFDLPVH
VHTHTDAGGQLATYFAAAQAGADAVIDGASAAPSGLTSOPSLSAIVAAFAHTRRDTGLS
LEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHIELPGQQLSNLRAQATALGLADRF
ELIEDNYAAVNEMLGRPTKVTPSSKXVUGDLALHLVAGVUDPADFAADPQKYDIPDSVII
AFLRGELGNPPGGWPEPLRTRALEGSEGKAPLTERVEPSEEQAHLDADDSKERRNSLNR
LLFPKPTEEFLERRFQNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISE
PDDKGMRNVAVNNGQIRPMVRDRSVEVTATAEKADSSNKGHVAAPFAGVVTVTA
EGDEVKAGDAVAILTEAMKMEATITASVDGKIDRVVYPAATKVEGGDLIVVVS"

Query Match 98.8%; Score 3578; DB 1; Length 3728;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	704	CAGTGCCTGGGACGGGTATGGGTTTGTGCTGAGCGCTTTCGGCATGGCGTATATG	763
Db	670	CAGTGCCTGGGACGGGTATGGGTTTGTGCTGAGCGCTTACCTGATGAGCTTCGCA	729
Qy	764	AATTAGCAACAGGATCTCGTGAAGCTGAAGCGCTTTCGGCATGGCGTATATG	823
Db	730	AATTAGCAACAGGATCTCGTGAAGCTGAAGCGCTTGGGATATGGGATATATG	789
Qy	824	TCGAACGGTGCTGATTAAACCTCAGGATATTGAAGTGCAGATCCTGGATCACACTG	883
Db	790	TCGAAACGGTGCTGATTAAACCTCAGGATATTGAAGTGCAGATCCTGGATCACACTG	849
Qy	884	GAGAAGTTGTACACCTTATGAACCGTCACTGCTCACTGCAGCGTCGTCAACAAAGTTG	943
Db	850	GAGAAGTTGTACACCTTATGAACCGTCACTGCTCACTGCAGCGTCGTCAACAAAGTTG	909
Qy	944	TCGAAATTGGCCAGCACCGATTGGATCCAGAACCTGGTGAATCGCATTTGGGATG	1003
Db	910	TCGAAATTGGCCAGCACCGATTGGATCCAGAACCTGGTGAATCGCATTTGGGATG	969
Qy	1004	CAGTAAGTTCTGGCTCCATGGTTACCGGGCGGGAAACCGTGGATTCTGGTCTG	1063
Db	970	CAGTAAGTTCTGGCTCCATGGTTACCGGGCGGGAAACCGTGGATTCTGGTCTG	1029
Qy	1064	ATGAAAAGGCCAACCGTCTTCAATCGAAATGAAACCCACCGTATCAGGTGAGCACCCG	1123
Db	1030	ATGAAAAGGCCAACCGTCTTCAATCGAAATGAAACCCACCGTATCAGGTGAGCACCCG	1089
Qy	1124	TGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCGAGATGGCCTGGCTGGTG	1183
Db	1090	TGACTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCGAGATGGCCTGGCTGGTG	1149
Qy	1184	CAACCTGAAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACCGGTGCAGGCACTG	1243
Db	1150	CAACCTGAAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACCGGTGCAGGCACTG	1209
Qy	1244	AGTGCCTACCCACCGGAAGATCCAACACGGCTTCCGCCACGATAACCGGAACATATCA	1303
Db	1210	AGTGCCTACCCACCGGAAGATCCAACACGGCTTCCGCCACGATAACCGGAACATATCA	1269
Qy	1304	CGCGTACCGCTCACCAAGGGAGCTGGCTCGTCTGACGGTGCAGCTCAGCTCGGGTG	1363
Db	1270	CGCGTACCGCTCACCAAGGGAGCTGGCTCGTCTGACGGTGCAGCTCAGCTCGGGTG	1329
Qy	1364	GGGAAATCACCGCACACTTGTGACTCCATGGTGAATAATGACCTGGCTGGCCGACT	1423
Db	1330	GGGAAATCACCGCACACTTGTGACTCCATGGTGAATAATGACCTGGCTGGCCGACT	1389
Qy	1424	TTGAAACTGCTGTTGCTCGTGCACAGCCGGCGGTGGCTGAGTTCACCGTGTGGTGTG	1483
Db	1390	TTGAAACTGCTGTTGCTCGTGCACAGCCGGGTGGCTGAGTTCACCGTGTGGTGTG	1449
Qy	1484	CAACCAACATTGGTTCTGGCTGGGGAAAGAGGAACCTTCCAAAGGCCA	1543
Db	1450	CAACCAACATTGGTTCTGGCTGGGGAAAGAGGAACCTTCCAAAGGCCA	1509
Qy	1544	TGGCCACCGGATTCCGATTCACCCGACCTCCCTCAGGCTCCACCTGATGATGATG	1603
Db	1510	TGGCCACCGGATTCCGATTCACCCGACCTCCCTCAGGCTCCACCTGATGATGATG	1569
Qy	1604	AGCAGGGACGGATTCCGATTCACCCGACCTCCCTCAGGCTCCACCTGATGATGATG	1663
Db	1570	AGCAGGGACGGATTCCGATTCACCCGACCTCCCTCAGGCTCCACCTGATGATGATG	1629
Qy	1664	GTCCAAAGGATGTTGCAAGCTCCATCGATAAGCTGCTGCAAGCCTCATGGTGTG	1723
Db	1630	GTCCAAAGGATGTTGCAAGCTCCATCGATAAGCTGCTGCAAGCCTCATGGTGTG	1689
Qy	1724	CACGCCGGTCCCGTGAACCGCCTGAAGCAAGCTGGCTGGCTGGCTGATCTCC	1783
Db	1690	CACGCCGGTCCCGTGAACCGCCTGAAGCAAGCTGGCTGGCTGATCTCC	1749
Qy	1784	GTGAGCAGGACGGCACTGGCAGTTACTGATAACCACCTTCGGGATGCACACCA	1843

Query	Match	Score	DB	Length
Query Match	98.8%	3578	DB 6	Length 3728;
Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;
Matches 3578;	Conservative	0;	Gaps 0;	
'	'	'	'	'
4 4	GCTTGAAGTCGTGCGGGTCAAGGTCAAGGGAGTGTGCCCCGAAACATTGAGAGGAACATGGAAACAAAAAAC	103	QY	
10	GCTTGAAGTCGTGCGGGTCAAGGTCAAGGGAGTGTGCCCCGAAACATTGAGAGGAACATGGAAACAAAAAAC	69	Db	
104	CGATGTTGATTGGGGATCTGGGTTACGATACTAGGACGGCAGTGACTGCTATCACCC	163	QY	
70	CGATGTTGATTGGGGATCTGGGTTACGATACTAGGACGGCAGTGACTGCTATCACCC	129	Db	
164	TTGGCGGTCTCTTGTGAAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGC	223	QY	
130	TTGGCGGTCTCTTGTGAAAGGAATAATTACTCTAGTGTGACTCACACATCTTCAACGC	189	Db	
224	TTCCAGCATTCAAAAGATCTTGGTAGCAAACCGGGGAATCGGGTCCGGTGCCTTCC	283	QY	
190	TTCCAGCATTCAAAAGATCTTGGTAGCAAACCGGGGAATCGGGTCCGGTGCCTTCC	249	Db	
284	GTGCAGCCTCGAACCCGGTGCAGGCCACGGTAGCTATTACCCCCGTGAAGATCGGGAT	343	QY	
250	GTGCAGCCTCGAACCCGGTGCAGGCCACGGTAGCTATTACCCCCGTGAAGATCGGGAT	309	Db	
344	CATTCCACCGCTCTTGTAAAGCTGTCCGCATGGTACCGAAGGCTCACCAAGTCA	403	QY	
310	CATTCCACCGCTCTTGTAAAGCTGTCCGCATGGTACCGAAGGCTCACCAAGTCA	369	Db	
404	AGGGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAGTAAGCAGATGCCA	463	QY	
370	AGGGTACCTGGACATCGATGAAATTATCGGTGCAGCTAAAGTAAGCAGATGCCA	429	Db	
464	TTTACCCGGGATACGGCTCCTGTGAAATTATCGATGGTCAACGGGAAAGGCTCACCA	523	QY	
430	TTTACCCGGGATACGGCTCCTGTGAAATTATCGATGGTCAACGGGAAAGGCTCACCA	489	Db	
524	ACGGCATTACTTTTATTGGCCAAACCCCAGGGCTCTGTGATCTCACCGGTGATAAGTCTC	583	QY	
490	ACGGCATTACTTTTATTGGCCAAACCCCAGGGCTCTGTGATCTCACCGGTGATAAGTCTC	549	Db	
584	GCGCGGTAAACGGCGGAGAAGGCTGGTCTGCCAGTTGGCCAGTAACTCCACCCGAGCA	643	QY	
550	GCGCGGTAAACGGCGGAGAAGGCTGGTCTGCCAGTTGGCCAGTAACTCCACCCGAGCA	609	Db	
644	AAAACATCGATGAGATCGTTAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGG	703	QY	
610	AAAACATCGATGAGATCGTTAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGG	669	Db	
704	CAGTGGCGGTGGTGGGGAGCGGGTATGCCGTTGGCTTCACTGTGAGCTTCGGCA	763	QY	
670	CAGTGGCGGTGGTGGGGAGCGGGTATGCCGTTGGCTTCACTGTGAGCTTCGGCA	729	Db	
764	AATTAGCAACAGAACCATCTCGTGAAGGCTGAAGGCCAGATGGGGGTATATG	823	QY	
730	AATTAGCAACAGAACCATCTCGTGAAGGCTGAAGGCCAGATGGGGGTATATG	789	Db	
824	TCGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	883	QY	
790	TCGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	849	Db	
884	GAGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	943	QY	
850	GAGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	909	Db	
944	TCGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	1003	QY	
910	TCGAACTGTTGACCTTATGAAACCTTACGATATTGAAACTGTCAGTGGCAGATCCTGGGATCACACTG	969	Db	
1004	CAGTAAAGTTCTGGCCAGCACGGATTGGATCCAGAACCTGGGGAAACCGTGTGAATTCTTGTGTC	1063	QY	
970	CAGTAAAGTTCTGGCCAGCACGGATTGGATCCAGAACCTGGGGAAACCGTGTGAATTCTTGTGTC	1029	Db	
2144	ACGGGCTTAACGAGCTCTCCAGATGGCTCCAGAACGGCAGTCAGCAGCAATCGACCA	2203	QY	

Db	70	CGATGTTGATTGGGGAACTGGACATACTAGGCACTGACTGTCAACCC	129	Qy	1244	AGTGGCGCATCACCAACAGGGCTTCGCCAGATAACGGAAACTATCA	1303
Qy	164	TGGCGGTCTTGTGAAAGGAATTAACTCTAGTGTGACTCACACATCTCAACGC	223	Db	1210	AGTGGCGCATCACCAACGGAAATCCAGGGAAACTATCA	1269
Db	130	TTGGCGGTCTTGTGAAAGGAATTAACTCTAGTGTGACTCACACATCTCAACGC	189	Qy	1304	CCGGTACCGCTCACAGGGGAGCTGGGTCTTGAGGGTAGCTCAGTCGGTG	1363
Qy	224	TTCAGGATTCAAAGATCTGGTAGCAACCGGGAAATCGGGTCCGTGCTTCC	283	Db	1270	CCGGTACCGCTCACAGGGGAGCTGGGTCTTGAGGGTAGCTCAGTCGGTG	1329
Db	190	TTCAGGATTCAAAGATCTGGTAGCAACCGGGAAATCGGGTCCGTGCTTCC	249	Qy	1364	GCGAAATCACCGCAACTTGAATGACTGCTGGTCAACCGTGTGGTGTG	1423
Qy	284	GTGCAACTCGAACCGGTGAGCTATTACCCCCGTGAAGATCGGGAT	343	Db	1330	GCGAAATCACCGCAACTTGAATGACTGCTGGTCAACCGTGTGGTGTG	1389
Db	250	GTGCAACTCGAACCGGTGAGCTATTACCCCCGTGAAGATCGGGAT	309	Qy	1424	TTGAAACTGCTGTTGCTGCAAGCGGGCTTGAGTTCACCGTGTGGTGTG	1483
Qy	344	CATTCCACCGCTCTTGTGAACTGGCATGGTACCGTACAGTCAGTCA	403	Db	1390	TTGAAACTGCTGTTGCTGCAAGCGGGCTTGAGTTCACCGTGTGGTGTG	1449
Db	310	CATTCCACCGCTCTTGTGTTGTGAACTGGCATGGTACCGTACAGTCA	369	Qy	1484	CAACCAAACATGGTTCTTGCTGGGGAAAGGGACTTCACCTCAAGGCCA	1543
Qy	404	AGCGTACCTGGACATCGATGAAATTATCGGTGAGCTAAAGCAAGATGCCA	463	Db	1450	CAACCAAACATGGTTCTTGCTGGGTGCTGCGGAAGAGGACTTCACCTCAAGGCCA	1509
Db	430	AGCGTACCTGGACATCGATGAAATTATCGGTGCAAGCTAAAAGTAAAGCAAGATGCCA	429	Qy	1544	TCGCCACCGGATTCAATTGGCGATCACCCGACCTCCCTCAAGGTCCACCTGCTGATGATG	1603
Qy	464	TTTACCCGGATAACGGCTTCTGTGAAATGCCAGCTTGGCGAGTTGGAAA	523	Db	1510	TCGCCACCGGATTCAATTGGCGATCACCCGACCTCCCTCAAGGTCCACCTGCTGATGATG	1569
Db	524	ACGGCATTAATCTTTATGGCCCACCCAGGGTTCTGTATCTCACCCGTGATAAGTCTC	583	Qy	1604	AGCAGGGACGGCATCCTGGATTACTTGGAGATGTCACCGTGAACAGGCTCATGGTGTG	1663
Qy	490	ACGGCATTAATCTTTATGGCCCAACCCCAGGGTTCTGTATCTCACCCGTGATAAGTCTC	549	Db	1570	AGCAGGGACGGATCTGGATTACTTGGAGATGTCACCGTGAACAGGCTCATGGTGTG	1629
Db	584	GCGGGTAACCGCCGGAAAGGGCTGCTGGCAGTTGGCGAAATCCACCCGAGCA	643	Qy	1664	GTCCAAGGGATGTTGCAAGCTCCATAGCTAACTCAAGGATCTGCCACTTGC	1723
Qy	644	AAAACATCGATGAGATCGTTAAAAGGGCTGTAAGGGCAAGCTTACCCATCTTGTGAAAGG	703	Db	1630	GTCCAAAGGGATGTTGCAAGCTCCATAGCTAACTCAAGGATCTGCCACTTGC	1689
Db	610	AAAACATCGATGAGATCGTTAAAAGGGCTGTAAGGGCAAGCTTACCCATCTTGTGAAAGG	669	Qy	1724	CACGGGTTCCCGTGAACGGCCCTGAAGCAGCTTCCGCGATGCCAACCGTCTCC	1783
Qy	704	CAGTGCCTGGCTGGGACGGGTTGGCTGCTGAAAGGGCTGTAAGGGCAAGCTTACCCATCTTGTGAAAGG	763	Db	1690	CACGGGTTCCCGTGAACGGCCCTGAAGCAGCTTCCGCGATGCCAACCGTCTCC	1749
Db	670	CAGTGCCTGGCTGGGACGGGTTGGCTGCTGAAAGGGCTGTAAGGGCTGTTGCTTACCCATCTTGTGAAAGG	729	Qy	1784	GTGAGCAGGGACTGGCTGCTGAAACCCACTGATAACCACCTTCCGGATGCCAACCGTCTCC	1843
Qy	764	AATTAGCAACAGAACATCTGTGAAAGCTGCTGAAAGGGCTTCCGGATGGCTTATATG	823	Db	1810	GTGAGCAGGGACTGGCTGCTGAAACCCACTGATAACCACCTTCCGGATGCCAACCGTCTCC	1869
Db	730	AATTAGCAACAGAACATCTGTGAAAGCTGCTGAAAGGGCTTCCGGATGGCTTATATG	789	Db	1750	GTGAGCAGGGACTGGCTGCTGAAACCCACTGATAACCACCTTCCGGATGCCAACCGTCTCC	1809
Qy	824	TCGAACGGCATTAACCCCTCAGGATATTGGAAAGCTGCTGAAAGGGCTTCCGGATGGCTTATATG	883	Qy	1844	CTCGCTGAGCTTTGTGCCCTGGGGCTCTGGCGACTACGATGGGGATGCCAACCGTCTCC	1903
Db	790	TCGAACGGCATTAACCCCTCAGGATATTGGAAAGCTGCTGAAAGGGCTTCCGGATGGCTTATATG	849	Db	1870	CTCGCTGAGCTTTGTGCCCTGGGGCTCTGGCGACTACGATGGGGATGCCAACCGTCTCC	1870
Qy	884	GAGAAAGTTGTACACCTTTATGAAAGCTGCTGAAACCAAAAAAGTTG	943	Qy	1904	CTCTGAGCTTTGTGCCCTGGGGCTCTGGCGACTACGATGGGGATGCCAACCGTCTCC	1963
Db	850	GAGAAAGTTGTACACCTTTATGAAAGCTGCTGAAACCAAAAGTTG	909	Db	1930	CTCTGAGCTTTGTGCCCTGGGGCTCTGGCGACTACGATGGGGATGCCAACCGTCTCC	1929
Qy	944	TCGAAAATGGCCAGCACGGCATTTGGAAACTGGCTGATCGCATTTGGGGATG	1003	Qy	1964	TCCTCTTGTGAGGATCCGGTGGGACAGGCTGCGGAGCTACGATGGGGATGCCAACCGTCTCC	2023
Db	910	TCGAAAATGGCCAGCACGGCATTTGGAAACTGGCTGATCGCATTTGGGGATG	969	Db	1990	TCCTCTTGTGAGGATCCGGTGGGACAGGCTGCGGAGCTACGATGGGGATGCCAACCGTCTCC	2049
Qy	1004	CAGTAAAGTTCTGGCTCCATGGTAACTGGCAACGGTGAATTCCTGGTG	1063	Qy	2084	TCTGCCGGCTTGGGAAAGCTGGCTCCGGCTGGGACATCTCCGCACTCTTC	2143
Db	970	CAGTAAGTTCTGGCTCCATGGTAACTGGCAACGGTGAATTCCTGGTG	1029	Db	2050	TCTGCCGGCTTGGGAAAGCTGGCTCCGGCTGGGACATCTCCGCACTCTTC	2109
Qy	1064	ATGAAAAGGGCAACACAGCTCTCATCGAAATGAACCCACGTATCAGGTGATGCCAACCG	1123	Qy	2144	ACCGCGCTTAAAGCAGCTCTGGGACATGCCAACCGTCTGGGAGGCCAACCA	2203
Db	1030	ATGAAAAGGGCAACACAGCTCTCATCGAAATGAACCCACGTATCAGGTGATGCCAACCG	1089	Db	2110	ACGGCGTTAAAGCAGCTCTGGGACATGCCAACCGTCTGGGAGGCCAACCA	2169
Qy	1124	TGACTGAAGATCACGGTGTGCTGACTGGCTGACTGGCTGATGCCAACCG	1243	Qy	2204	CCGGGGTAGCCAGGGGAGCTGGCTATGGCTTATCTGATCCAATGAAAAGC	2263
Db	1090	TGACTGAAGATCACGGTGTGCTGACTGGCTGACTGGCTGATGCCAACCG	1149	Db	2170	CCGGGGTAGCCAGGGGAGCTGGCTATGGCTTATCTGATCCAATGAAAAGC	2289
Qy	1184	CAACCTTGAAGGAATTGGGATTACTACCTAAAGATGGCAAGGGAGATCGTCAAGTCTGGGCTCACA	2323	Qy	2230	TCTACACCCCTGGATTACTACCTAAAGATGGCAAGGGAGATCGTCAAGTCTGGGCTCACA	2209
Db	1150	CAACCTTGAAGGAATTGGGATTACTACCTAAAGATGGCAAGGGAGATCGTCAAGTCTGGGCTCACA	1209				

2324 TCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCGCCAGCTGGGTAAACCAAGCTGGTCA 2383 Db Db 3370 CCTCAACAAAGGCCATGTGCTGCACCATCGTGTGACTGGTCA 3429

2290 TCTTGGCCATTAAAGGATATGGCTGGTCTGCTTCGCCAGCTGGGTAAACCAAGCTGGTCA 2349 Qy Qy 3464 AAGGTGATGAGGTCAAGGTGGAGATGCACTGGTCA 3523

2384 CGGCACTGGCCAGTTCGATCTGCCAAGTGGCACACCCAGGAACTGGGGTG 2443 Db Db 3430 AAGGTGATGAGGTCAAGGTGGAGATGCACTGGTCA 3489

2350 CGGCACTGGCCAGTTCGATCTGCCAAGTGGCACACCCAGGAACTGGGGTG 2409 Qy Qy 3524 CAACAACTACTGCTTCTGTGACGGCAAATCGMTCGGTGCTGCAACGA 3583

2444 GCCAGCTGGCAACCTTAACCTTGCTGAGCTAACGCTGGTGGAGATGGTGTGACGGTCT 2503 Db Db 3490 CAACAACTACTGCTTCTGTGACGGCAAATCGMTCGGTGCTGCAACGA 3549

2410 GCGAGCTGGCAACCTTAACCTTGCTGAGCTAACGCTGGTGGAGATGGTGTGACGGTCT 2469 Qy Qy 3584 AGGTGAGGTGGGACTTGAATGGTGTGACGGCAAATCGMTCGGTGCTGCAACGA 3621

2504 CCGGACCACTGTCTGGGACCACTCCCAGCCATCCTGCTGCAATTGTGCTGCAATTG 2563 Db Db 3550 AGGTGAGGTGGGACTTGAATGGTGTGCTGCAACGA 3587

2470 CGGACCACTGTCTGGGACCACTCCCAGCCATCCTGCTGCAATTGTGCTGCAATTG 2529 Qy Qy RESULT 9

2564 CGCACACCGTGGGATAACGGTTGAGCCTCGAGGCTGTTCTGACCTCGAGGGTACT 2623 Db Db AF503915 3657 bp DNA linear BCT 13-MAY-2002

2530 CGCACACCGTGGGATAACGGTTGAGCCTCGAGGCTGTTCTGACCTCGAGGGTACT 2589 LOCUS Corynebacterium crenatum strain CD945 pyruvate carboxylase (pyc)

2624 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2683 DEFINITION Corynebacterium crenatum gene, complete cds.

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 ACCESSION AF503915

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 VERSION AF503915.1 GI:20531756

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 KEYWORDS Corynebacterium crenatum

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 SOURCE Corynebacterium crenatum

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 ORGANISM Corynebacterium crenatum

2590 GGGAAAGCA GTGCGGGAGCTGTACTGCCATTGAGTCGGAAACCCAGGCCAACGGTC 2649 Bacteria; Actinobacteria; Actinomycetales; Corynebacterium.

2744 CACTGGGCCTTGCAGATCGAAAGACAATACGAGCTTCCAAACCTGGCTTAATGAGA 2743 Qy Qy REFERENCE 1 (bases 1 to 3657)

2650 CACTGGGCCTTGCAGATCGAAAGACAATACGAGCTTCCAAACCTGGCTTAATGAGA 2709 AUTHORS Wang, J., Ding, J. and Liu, Y.

2710 CACTGGGCCTTGCAGATCGAAAGACAATACGAGCTTCCAAACCTGGCTTAATGAGA 2769 TITLE Cloning and Expression of Pyruvate Carboxylase Gene in

2804 TGCTGGGACGGCCAAACCAAGGTACCCCATCTCAAGGTGTCGACCTCGCACTCC 2863 Db Db Corynebacterium crenatum Unpublished

2770 TGCTGGGACGGCCAAACCAAGGTACCCCATCTCAAGGTGTCGACCTCGCACTCC 2829 JOURNAL Wang, J., Ding, J. and Liu, Y.

2864 ACCTCTGGTGGTGGGACTTGGGATCCAGGAGACTTGGCTGCCATCACAAAGTAGGACA 2923 Db Db DIRECT SUBMISSION Wang, J., Ding, J. and Liu, Y.

2830 ACCTCTGGTGGTGGGATCCAGGAGACTTGGCTGCCATCACAAAGTAGGACA 2889 JOURNAL Submitted (18-APR-2002) Center of Microbial Biotechnology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100080, China

2924 TCCCCAGACTCTGTATCGGTTCCAGGTGGCTGGC 2983 JOURNAL Location/Qualifiers

2890 TCCAGACACTGTGTCATCGGTTCCAGGTGGCTGGC 2949 JOURNAL 1. 3657 (bases 1 to 3657)

Db Db 1. 3657 /product="Corynebacterium crenatum"

2890 TCCAGACACTGTGTCATCGGTTCCAGGTGGCTGGC 2829 JOURNAL /mol_type="genomic DNA"

2984 CAGAGCCACTGGCACCCGGCACTGGAAAGGCCACCTCTGACGG 3043 JOURNAL /strain="CD945"

2950 CAGAGCCACTGGCACCCGGCACTGGAAAGGCCACCTCTGACGG 3009 JOURNAL /db_xref="taxon:168810"

3044 AAGTTCCCTGGGAAGGAGCACCGGCACTGGAAAGGCCACCTCTGACGG 3103 JOURNAL 151. .3573 /gene="pyc"

Db Db /codon_start=1 /product="pyruvate carboxylase"

3010 AAGTTCCCTGGGAAGGAGCACCGGCACTCTGACGGCTGATGATTCCAAGGAACGTGCAATA 3069 JOURNAL /protein_id="AAM27458.1"

3104 GCCTCAACCCGCTGCTGTTCCCGAACCGGAAGAGGTCTCTGAGGCCCGCT 3163 JOURNAL /db_xref="GI:20531757"

3070 GCCTCAACCCGCTGCTGTTCCCGAACCGGAAGAGTCTCTGAGGCCCGCT 3129 JOURNAL /translation="MSTHTTSSTLPAFKKKILVANRGEIAVRAFRAALETGAATVAIYPR EDRGSPHRSFASEAVRIGTEGSPVKAYLDIILIGAKKVRADAIYPPGYFLSENAQL ARECBAENGTFIGPTGPVLDLITQPSDKEVLRLKLAESTPSKNIDIVKSAEG QTYPIFYKAVAGGGGRGMRFVSSPDELRCSLQRRHOKVYELAPAQHLDPELRDRICADA VEQQLGDRTGEVVHLYERDCSLLRPAQHLDPELRDRICADA VPKFCRSI GYOGAGTVEFLVDEKGNTHTVFLQGPAAPARDREQLDAVTDLVKAQMRLAAGTILKEL GLTQDKIKITHGAAQLCRITTEDPNNGFRPDGTGTTAYRSPGAGAVRLDGAQLGGEIT AHFDMSMLYQOMTCRGSDFETAVARAORALAABFTVSQVATNIGFLRALLREEDFTSKRIRIA TGFELJDHPHLLQAPPADDEOGRILDLADVTVNPKPHGVPRKDVAAPIDKLPNLPL PRGSRDRLLQGPAAPARDREQLDAVTDLVKAQMRLAAGTILKEL KLTPELSSVEAWNGQATDVAIRPLFEDPWRDRLLDQSLIATRVSFAALKPAAEAVA YPDSCVCRAFVKEAATSGVDIFRIFDALNDVSOMRPAIDAVLENTAVAEVAMAYSGDL SDPNEKLYTLDYILKMAEIVKSGAHILLAIKDMAGLRLPAATKLVTLARREFDLPVH VHTHDAGQQLATYFAAQAGQADAVDGASAPLSGTTQSPLSIAVAAFAHTRRDGELS LEAVSDLEPYWEAVRGLYLPPFESGTGPPTGPRVYRHEIPGGOLSNLRAQATALGLADRF ELLIEDNYAAVNEMIIGRPTKVTPSSKVGDLALHLVAGVDEADFADFAADPQKYDIPDSVI AFLRGERGLGNPGGWPEPLTRALEGRSEGGKAPLTEVPEEEQAHLDADDSKERRNSLNR LLFPKPTEFFLEHRRRERGNTISALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISE PDDKGMRNVVANVNGQIRPMVRDRSVESTATAEKADSSNKGHVAAPFAGVVTVTVA

3224 AGACTTGTGATCCGGCTGCCAGATGTGGCAACCCCAACTGCTTGTGGATGGCATCT 3283 Qy Qy

3164 TCGGCAACACCCCTCTGGCTGGATGATGTCGTTCTACGGCTGGTCAAGGCCGG 3223 Db Db

3130 TCGGCAACACCTCTGGCTGGATGATGTCGTTCTACGGCTGGTCAAGGCCGG 3189

3284 CTGAGGCCAGGATAAGGGTATGGCAATGGCCAACTGCTTGTGGCAACGGCCAGATCGGCC 3343

3250 CTGAGGCCAGGATAAGGGTATGGCAATGGCAACGGCCAGATCGGCC 3309

3344 CAATGGCTGTGGCTGCCAGATGTGGCAACCCCAACTGCTTGTGGATGGCATCT 3403

3310 CAATGGCTGTGGCTGCCAGATGTGGCAACGGCCAGATCGGCC 3369

3404 CCTCCAAACAAAGGCCATGTGGTCAACCGTACTGGTCAACCGCAACGGCAGATT 3463

EGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAATKVEGGDLIVVIS"

ORIGIN	Query	Match	Score	Length	DB	No.	QY	1069	AAGGGCAACCACTCGTCTCATCGAAATGAACCCAGTATCCAGGTGACT
		95.8% ; Matches 3508 ; Best Local Similarity	3469 ; Pred. No. 0 ; Mismatches 65 ; Indels 0 ; Gaps 0 ;	3657 ;	1	1021	AAGGGCAACCACTCGTCTCATCGAAATGAACCCAGTATCCAGGTGACT	1080	
		98.2% ; Conservative	0 ;						
		49	AAGTCGTGAGGTCAGGGGACTGTTGCCGAAAACATGAGGAAAACACCGATG	108		1129	GAAGAAGTCACCGAGGTGAGCTGGCTTGCGCAGATGGCTTGGCTGCAACC	1188	
		1	AACTCGTGCAGGTAGGGAGTGGCCGAAACATGAGGAAAACACCGATG	60		1081	GAAGAAGTCACCGAGGTGAGCTGGCTTGCGCAGATGGCTTGGCTGCAACC	1140	
		109	TTTGATTGGGGAAATGGGGGATTAATTACTCTAGGACCGAGTGA	168		1189	TGAGAGGAATTGGGTCTGACCCAAAGATAAGATAAGAACCCAGGTGAGCTG	1248	
		61	TGGCTCTGGGGAAATGGGGGATGGGGTACAGATACTAGGACCGAGTGA	120		1141	TGAGAGGAATTGGGTCTGACCCAAAGATAAGATAAGAACCCAGGTGAGCTG	1200	
		169	GGTCTCTGGTTGAAAGGAATAATTACTCTAGGACCGAGTGA	228		1249	CGCATCACCCACGGGAAAGATAACGGGAAACTATCACCGCG	1308	
		121	GGTCTCTGGGGAAATGGGGGATGGGGTACAGATACTAGGACCGAGTGA	180		1201	CGCATCACCCACGGGAAAGATAACGGGAAACTATCACCGCG	1260	
		229	GCATTCAAAAAGATCTTGGTAGCAAACCGGGGAAATTCGGGTGCA	288		1309	TACCGCTCACCCAGGGGGAGCTGGTTCTGACGGGTGAGCTCAGGCTCGGTGGCGAA	1368	
		181	GCATTCAAAAAGATCTTGGTAGCAAACCGGGGAAATTCGGGTGCA	240		1261	TACCGCTCACCCAGGGGGAGCTGGCTTCTGACGGGTGAGCTCAGGCTCGGTGGCGAA	1320	
		289	GCACTCGAAAACCGGGTCAAGCCACGGTAGCTATTACCCCCGTGA	348		1369	ATCACCGCACAATTGACTCCATGTTGAAATAATGACCTTGGCTTCCGACTTTGAA	1428	
		241	GCACTCGAAAACCGGGTCAAGCCACGGTAGCTATTACCCCCGTGA	300		1321	ATCACCGCACAATTGACTCCATGTTGAAATAATGACCTTGGCTTCCGACTTTGAA	1380	
		349	CACCGCTCTTTGCTCTGAAAGCTGGTACCGAAGGGCTTACCAAGTCAGGG	408		1429	ACTGCTGTTGCTCGTGCACAGGGGGCTTGGCTGAGTTCACTGGTGTGAA	1488	
		301	CACCGCTCTTTGCTCTGAAAGCTGGTACCGTCAAGGG	360		1381	ACTGCTGTTGCTCGTGCACAGGGGGCTTGGCTGAGTTCACTGGTGTGAA	1440	
		409	TACCTGGACATCGATGAAATTATCGGTGCAAGCTAAAGGATGCCATTAC	468		1489	AAACATTGGTTCTTGGCTGAGTTCACTGGTGTGAAAGGACTTCACTTCCAAAGGCATCGCC	1548	
		361	TACCTGGACATCGATGAAATTATCGGTGCAAGCTAAAGGATGTTATTAC	420		1501	AAACATTGGTTCTTGGCTGAGTTCACTGGCTCACCTGGGATGATGAGCGAG	1500	
		469	CCGGGATACGGCTTCCTGTCGAAAATGCCAGCTGGGGAAAACGGC	528		1549	ACGGGATTCCCGGATCACCCGCTCAGGCTCAGCTGGCTGAGCGAG	1608	
		421	CCGGGATATGGCTTCCTGTCGAAAATGCCAGCTGGGGAAAACGGC	480		1501	ACGGGATTCCCGGATCACCCGACACCTCTTCAAGGCTCACCTGGGATGAGCGAG	1560	
		529	ATTACTTTATTGGCCAACCCAGGGTTCTGATCTCGGGG	588		1609	GGAAAGGCATCCGGCTCTATCGATAAGTGTGCCACTTGCACAGC	1668	
		481	ATTACTTTATTGGCCAACCCAGGGTTCTGATCTCGGGTATAAGTCTGTGCG	540		1621	AAAGGATGTTGAGGACCCATTGCGATAAGTGTGCCACTTGCACAGC	1620	
		589	GTAACCCGGGAAGAAGGGCTGTAAAGGCTGAAGGGCCAGACTTACCCATC	648		1669	AAGGATGTTGAGGACCCATTGCGATAAGTGTGCCACTTGCACAGC	1728	
		601	GTAACCCGGGGAAAGGGCTGTAAAGGCTGAAGGGCCAGACTTACCCATC	660		1621	AAAGGATGTTGAGGACCCATTGCGATAAGTGTGCCACTTGCACAGC	1680	
		649	ATCGATGAGATGTTAAAGGGCTGAAGGGCCAGACTTACCCATC	708		1729	GSTTCCCGTGAACCGGCTGAAAGGAGCTGGCTTGGCTGATCTCCGTGAG	1788	
		601	ATCGATGAGATGTTAAAGGGCTGAAGGGCCAGACTTACCCATC	660		1681	GGTCCCGTGAACCGGCTGAAAGGAGCTGGCTTGGCTGATCTCCGTGAG	1740	
		709	GCCGGGTGGGGAAACGGCTGTGGTTGTTGCTTACCTGATGAGCTGAA	768		1789	CAGGACGGACTGGCAGTTACTGATAACCCACCTTCCGGATGAC	1848	
		661	GCCGGGTGGGGAAACGGCTGTGGTTGTTCTTACCTGATGAGCTGAA	720		1741	ACCGGAGTCCGCTCATTCGGCTGAGTTACTGATAACCCACCTTCCGGATGAC	1800	
		769	GCAACAGAAGCATTCTGGTAAGGCTGAAGGGCTGGGTATATGTCGAA	828		1849	GGCTTTGGTCCGCTCATTCGGCTGAGTTACTGATAACCCACCTTCCGGATGAC	1908	
		721	GCAACAGAAGCATTCTGGTAAGGCTGAAGGGCTGGGTATATGTCGAA	780		1801	ACCGGAGTCCGCTCATTCGGCTGAGTTACTGATAACCCACCTTCCGGATGAC	1860	
		829	CGTGTGTGATAACCCCTCAGCATATTGAAAGTGTGAAGGGCATC	888		1909	GAGCTTTGGTCCGCTCATTCGGCTGAGTTACTGATAACCCACCTTCCGGATGAC	1968	
		781	CGTGTGTGATAACCCCTTATGAAAGTGTGAAGGGCATC	840		1861	GAGCTTTGGTCCGCTCATTCGGCTGAGTTACTGATAACCCACCTTCCGGATGAC	1920	
		889	GTTGTACACCTTATGAAAGTGTGAAGGGCATC	948		1969	TTTGGGATCCTGGGACAGGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCT	2028	
		841	GTTGTACACCTTATGAAAGTGTGAAGGGCATC	900		1921	TTTGGGATCCTGGGACAGGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCT	1980	
		949	ATTGGCGCAGCACGGCATTTGGTCACTGGCTGAGCTGGCTGAGCTGG	2148		2029	CAGATGCTGTTGGTAAAGGAAGCTGGCTGGGACATCTTCCGATCTTCGACCG	2088	
		901	ATTGGCGCAGCACGGCATTTGGTCACTGGCTGAGCTGGCTGAGCTGG	2100		1981	CAGATGCTGTTGGTAAAGGAAGCTGGCTGGGACATACCCAGACTCCG	2040	
		1009	AAGTTCGCTCCATTGGTACAGGGGGAAACCGGGGGAAATTCTTGGGATGAA	1068		2041	CGGGCGGTTGGTAAAGGAAGCTGGCTGGGACATCTTCCGATCTTCGACCG	2148	

QY	439	GCTAAAAAAGTAAAGCAGATGCCATTACCGGGATA CGGTTCTGTCAAATGCC 4 98	Db	1321	GAAGAGGACTTCACTRCAAGGCATCGCCACCGGATTCA TGCATGCCGATCACCCGCACCTC 1380
Db	241	GCTAAAAAAGTAAAGCAGATGCCATTACCGGGATA CGGTTCTGTCAAATGCC 3 00	QY	1579	CTTCAGGCTCACCCTGCTGATGATGTTACTTGGGATTACTTGGGATGATGAGATGTC 1638
QY	499	CAGCTTGCCTCGGAGTGTGCGAAAACGGCAATTACTTTATTGGCCAACCCCAGGGTT 558	Db	1381	CTTCAGGCTCACCCTGCTGATGAGGGCAAGGGATGTC 1440
Db	301	CAGCTTGCCTCGGAGTGTGCGAAAACGGCAATTACTTTATTGGCCAACCCCAGGGTT 3 60	QY	1639	ACCGTGAACAGGCTCATGGTGCAGTCCTATCGATAAGCTG 1698
QY	559	CTTGATCTCACCGGTATAAGTCTCGCCGTAACCGCCGGAAAGAAGGCTGTCGCCA 618	Db	1441	ACCGTGAACAGGCTCATGGTGCAGTCCTATCGATAAGCTG 1500
Db	361	CTTGATCTCACCGGTATAAGTCTCGCCGTAACCGCCGGTAACCGCCGGAAAGAAGGCTGTCGCCA 420	QY	1699	CCTAACATCAAGGATCTGGCACTGCCACGGGTTCGGCTGAAAGCAGCTGGC 1758
QY	619	GTTTTGGGAAATCACCGGTAAACAAACATCGATGAGATCGTAAAGGGCTGAAGGC 678	Db	1501	CCTAACATCAAGGATCTGGCACTGCCACGGGTCCGGTACGGACTGACCC 1560
Db	421	GTTTTGGGAAATCACCGGTAAACAAACATCGATGAGATCGTAAAGGGCTGAAGGC 480	QY	1759	TTCAGCGGATCACAGGACTGGCAACTGCCACGGGTTCGGCTCATTGGCACTGAAAGCCT 1818
QY	679	CAGACTTACCCCCATCTTGTGAAGGCAGTGGCGGTATGCGTT 738	Db	1561	CCAGCGCATTGCTGATCTGGCACTGCCAGTGGCAACTGACCC 1620
Db	481	CAGACTTACCCCCATCTTGTGAAGGCAGTGGCGGTATGCGTTAAAGGGCTGAAGGC 540	QY	1819	TTCAGCGGATCACAGGACTCTGGCTGATGCTGAAAGCTGGCACTGAAAGCCT 1878
QY	739	GTTGCTTACCTGTAGGCTTCGCAATTAGCAACAGAACATCTCGTGAAGCTGAAGGC 798	Db	1621	TTCAGCGGATCACAGTGGCACTGCCAGTGGCAACTGACCC 1620
Db	541	GTTGCTTACCTGTAGGCTTCGCAATTAGCAACAGAACATCTCGTGAAGCTGAAGGC 600	QY	1879	GGGGAGAGGGGATGGCAAGAGCTGACTCTGGAGGGCTTGGCAAGGGCTGACGAG 1938
QY	799	GCTTTCGGGATGGGGATCACACTGGGTTATGTGAACTTCTCAGGATATTGAA 858	Db	1681	GGGGAGAGGGGATGGCAAGGGCTTGGCAAGGGCTGGGG 1740
Db	601	GCTTTCGGGATGGGGTATATGTGAACTTCTCAGGATATTGAA 660	QY	1939	GCGACCTACAGGATGGGGATGGGATGCGGTTCTCTGGGACAGGGCTGACGAG 1998
QY	859	GTGGAGATCCTGGGATCACACTGGGTTATGTGAACTTCTCAGGATTTGCTCA 918	Db	1741	GCGACCTACAGGATGGGGATGGGATGCGGTTCTCTGGGACAGGGCTGACGAG 1800
Db	661	GTGAGATCCTGGGATCACACTGGGAAATTGTGAACTTCTCAGGATATTGAA 720	QY	1999	CTGGCGAGGGGATGCCGAAATGTAACATTCAAGATGGCAAGCTGGCAACCGGTG 2058
QY	919	CTGGAGCTGCTGTCACCAAAAGTTGTGAAATTGGCAGCACAGCATTGGATCCAGAA 978	Db	1801	CTGGCGAGGGGATGCCGAAATGTAACATTCAAGATGGCAAGCTGGCAACCGGTG 2058
Db	721	CTGGAGCTGCTGTCACCAAAAGTTGTGCAAAATTGGCAGCACAGCATTGGATCCAGAA 780	QY	2059	GGATACACCCGTAACCGAGACTCCGCTGCGGGGTTAAGGAAGCTGTCAGGCC 2118
QY	979	CTGGCTGATCGCATTTGGGATCACCAAAAGTTGTGAAATTGGCAGCACAGCATTGGATCCAGAA 1038	Db	1861	GGATAACCCGTAACCAAGCTCCGATCTGGCTTCTGGGATGGCTGGG 2178
Db	781	CTGGCTGATCGCATTTGTGGGATGCAGTAAGTTGTGCAAAATTGGTACCGGGC 840	QY	2119	GGCGTGGACATCTTCGCGATCTCCGATCTGGCTTCTGGGATGGCTGGG 2178
QY	1039	GCGGAAACCGTGAATTCTGGTCACTGGTAAAGTTGTGCAACCGTCTCATGAAATGCAAC 1098	Db	1921	GGCGTGGACATCTTCGCGATCTGGCTTCTGGGATGGCTGGG 2178
Db	841	GCGGAAACCGTGAATTCTGGTCACTGGTAAAGTTGTGCAACCGTCTCATGAAATGCAAC 900	QY	2179	ATCGAGCGAGCTGGAGACCAAAACCGGGTAGCCGAGGTGGCTATGGCTTATTCTGGT 2238
QY	1099	CCACGTTACCCAGGTTGAGCACCCGTGACTGAAAGATCACCGGGTTGGACCTGGTCAAG 1158	Db	1981	ATCGAGCGAGCTGGGATCTGGGAGGGCTATGGCTGGG 2040
Db	901	CCACGTTACCCAGGTTGAGCACCCGTGACTGAAAGATCACCGGGTTGGACCTGGTCAAG 960	QY	2239	GATCTCTCTGATCCAATGAAAGCTCAACCCGTTAAGGATATGGCTGGG 2298
QY	1159	GCGCAGATTCGGCTGGCTGGTGTGCAACTTGTGAAAGGAAATTGGGATGGCTGAG 1218	Db	2041	GATCTCTCTGATCCAATGAAAGCTCAACCCGTTAAGGATATGGCTGGG 2100
Db	961	GCGCAGATTCGGCTGGCTGGTGTGCAACTTGTGAAAGGAAATTGGGATGGCTGAG 1020	QY	2299	GAGATCGTCAAGTCTGGGCTCACATTGGGATGGCTGGG 2298
QY	1219	ATCAAGACCCACGGCTGGCAGCACTGGCTGCGCATCACCAACGGAAAGATCAACGGGC 1278	Db	2101	GAGATCGTCAAGTCTGGGCTCACATTGGGATGGCTGGG 2220
Db	1021	ATCAAGACCCACGGCTGGCAGCACTGGCTGCGCATCACCAACGGAAAGATCAACGGGC 1080	QY	2359	CCAGCTGGGTAACCAAGCTGGCTGCACTGGCCACCGGACTGGCTGGG 2418
QY	1279	TTCGGCCAGATACCGGAACATTACCGGCTACCCGCACTGGCTGGG 1338	Db	2161	CCAGCTGGGTAACCAAGCTGGCTGCACTGGCCACCGGACTGGCTGGG 2418
Db	1081	TTCGGCCAGATACCGGAACATTACCGGCTACCCGCACTGGCTGGG 1140	QY	2419	GTGCACACCCAGGACACTGGCTGGCCAGCTGGCTGGCTGGCACTGGCTGGC 2478
QY	1339	CTTGACGGCTCAGCTGCTGGTGTGGCTGGCTGGCAACACTTGTGACTGCCATGGTCAAGCT 2280	Db	2221	GTGCACACCCAGGACACTGGCTGGCTGGCAACCTACTGGCTGGCTGGCACTGGCTGGC 2280
Db	1141	CTTGACGGCTCAGCTGCTGGTGTGGCTGGCTGGCAACACTTGTGACTGCCATGGCTGGC 2200	QY	2479	GGTGCAGATGCTGGTGTGGCTGGCAACACTGGCTGGCTGGCAACCTGGCTGGC 2538
QY	1399	AAAATGAACTCTGGCTGGTGTGGCTGGCAACACTTGTGACTGCCATGGCTGGC 1458	Db	2281	GGTGCAGATGCTGGTGTGGCTGGCAACACTGGCTGGCTGGCAACCTGGCTGGC 2340
Db	1201	AAAATGAACTCTGGCTGGTGTGGCTGGCAACACTTGTGACTGCCATGGCTGGC 1260	QY	2539	CTGTCTGCCATTGGTGTGGCTGGCAACACTGGCTGGCTGGCAACCTGGCTGGC 2598
QY	1459	GCTGAGTTCACCGTGTGGTGTGGCTGGCTGGCTGGCAACACTGGCTGGC 1518	Db	2341	CTGTCTGCCATTGGTGTGGCTGGCTGGCAACACTGGCTGGCTGGCAACCTGGCTGGC 2400
Db	1261	GCTGAGTTCACCGTGTGGCTGGCAACACTTGTGCTGGCTGGCTGGC 1320	QY	2599	GCTGTTTCTGACCTCGGAAAGCAACTGGCTGGCAACACTGGCTGGC 1578
QY	1519	GAAGAGGACTTCACCTCCAAAGGGCACTCGCACCCGCAACCTGGCTGGCAACCTGGC 1578			

2401	GCTGTTCTGACCTCGAGCGTACTGGAAAGCAGTGGGGACTGTACCTGCCATTGAG	2460	JP 2002191370-A/765.
2659	TCTGGAACCCCAAGGCCAACCCGGTCTACCGGAATCCACGGAAATCCAGGGGACAGTTG	2718	KEYWORDS SOURCE ORGANISM
b	TCTGGAACCCCAAGGCCAACCCGGTCTACCGGAATCCAGGGGACAGTTG	2520	unclassified
2719	TCCAACCTGGGTGCACAGGCCAACCGGCACTGGGCTTTCGAACCTCATCGAA	2778	REFERENCE AUTHORS
y	TCCAACCTGGGTCTACCGGAATCCAGGGGACAGTTTCGAACCTCATCGAA	2580	Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A.
b	TCCAACCTGGGTCAACGGCACTGGGCTTGGGATCGTTTCGAACCTCATCGAA	2779	TITLE JOURNAL
y	TCCAACCTGGGTCAACGGCACTGGGCTTGGGATCGTTTCGAACCTCATCGAA	2838	Novel polynucleotide Patent: JP 2002191370-A 765 09-JUL-2002;
b	GACAACTA CGCAGGCCAACCAAGGTCA CCCCCATCCTCC	2898	COMMENT
y	GACAACTA CGCAGGCCAACCAAGGTCA CCCCCATCCTCC	2640	KYOWA HAKKO KOGYO CO LTD
b	AAGGTTGGGACCTCGCACTCGTGGATGCTGGGGTGTGAGCTTT	2700	OS Corynebacterium glutamicum
y	AAGGTTGGGACCTCGCACTCCACCTCGTGGGGTGTGAGCTTT	2700	PN JP 2002191370-A/765
b	GCTGCCGATCCACAAAAGTAGCACATCCCAGACTCTGTCATCGGTTCCCTGCGGGGAG	2958	PD 09-JUL-2002
y	GCTGCCGATCCACAAAAGTAGCACATCCCAGACTCTGTCATCGGTTCCCTGCGGGGAG	2760	PF 15-DEC-2000 JP 2000405096
b	CTTGGTAACCCTCCAGGTGCTGGCCAGGGCCACTTGCA CCCGGCAGTGGCACCCGGC 3018	2701	PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI, KEIKO OCHIAI, HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO OZAKI
y	CTTGGTAACCCTCCAGGTGCTGGCCAGGGCCACTTGCA CCCGGCAGTGGCACCCGGC 2820	2959	PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC C12N1/15,
b	TCCGAAGGCCAACCTCTGACGGAAAGTCCCTGAGGAAGAGCCACCTCGACCGCT 3078	3019	PC C12N1/19, C12N5/10, C12N9/00, C12P7/40, C12P13/04, C12P13/08, C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC G01N33/566
y	TCCGAAGGCCAACCTCTGACGGAAAGTCCCTGAGGAAGAGCCACCTCGACCGCT 2880	2761	PC G01N33/569, G01N33/68, G01N37/00, /C12P21/08, (C12N1/21, C12R1:13), (C12N1/21, C12R1:01), (C12N1/21, C12R1:15), PC C12N5/00, C12N15/00, PC C12N5/00, C12N15/00
b	3079 GATGATCCAAGGAACCGCACCTCTGACGGAAAGTCCCTGAGGAAGAGCCAAACCGAA 3138	2821	CC Novel polynucleotide
y	2881 GATGATCCAAGGAACCGCACCTCTGACGGAAAGTCCCTGAGGAAGAGCCAAACCGAA 2940	FT FT	Key Location/Qualifiers
b	3139 GAGTTCTCGAGGCCAACCGTCCGCTGGATGATCGTGAATTTC 3198	2941	Source 1. .3420
y	2941 GAGTTCTCGAGGCCAACCGTCCGCTGGATGATCGTGAATTTC 3000	FEATURES	/organism='Corynebacterium glutamicum'.
b	3199 TTCTACGGCCTGGTCGAAGGCCGAGACTTGTATCCGCCATGGTGGCACCCCA 3258	ORIGIN	source 1. .3420
y	3001 TTCTACGGCCTGGTCGAAGGCCGAGACTTGTATCCGCCATGGTGGCACCCCA 3060	Query Match	/organism='genomic DNA'
b	CTGCTTGGCTGGATGGGATCTCTGAGCCAGACCGATAAGGGTATGCGCAATGGTGTG 3318	Best Local Similarity	/db_xref="taxon:32644"
y	3061 CTGCTTGGCTGGATGGGATCTCTGAGCCAGACCGATAAGGGTATGCGCAATGGTGTG 3120	Matches 3420;	0; Mismatches 0; Indels 0; Gaps 0;
b	3319 GCCAACGGTCAACGGCAGATCCGCCAACACCGCTTCGGCTGGATGAGCTGTGTC 3378	QY	199 GTGTGACTCACACATCTCACCGCTTCCAGCATCAAAGAGATCTTGGTAGCAAACCGC 258
y	3121 GCCAACGGTCAACGGCAGATCCGCCAACACCGCTTCGGCTGGATGAGCTGTGTC 3180	Db	1 GTGTGACTCACACATCTCACCGCTTCCAGCATCAAAGAGATCTTGGTAGCAAACCGC 60
b	3379 ACCGGCAACGGCAAGGGCAGATTCTCCAAACAGGGCCATGGTGGCTGGCACCCATTGGCT 3438	QY	259 GGCGAAATCGCGGTCCGGTGTGAGCAGCTCGAAACCGGTGAGCCACCTCGTGGTAGCT 318
y	3181 ACCGGCAACGGCAAGGGCAGATTCTCCAAACAGGGCCATGGTGGCTGGATGAGCTGTGTC 3240	Db	61 GGCGAAATCGCGGTCCGGTGTGAGCAGATCGGGGATCATCCACCGGCTTTCGGTAGCT 120
b	3439 GGTGTTGACTCGAGCTGGCTGAAGGTGATGAGGTCAAGGCTGGGACTTGAGTCGGT 3498	QY	319 ATTACCCCGTGAAGAGATCGGGGATCATCCACCGGCTCTTGGCTGAAGGCTGTCCGC 378
y	3241 GGTGTTGACTCGAGCTGGCTGAAGGTGATGAGGTCAAGGCTGGGACTTGAGTCGGT 3300	Db	121 ATTACCCCGTGAAGAGATCGGGGATCATCCACCGGCTCTTGGCTGAAGGCTGTCCGC 180
b	3499 ATCATCGAGGCTATGAAGATGGAAAGCAAAATCACTGGCTTCGGTGAACCCATTGGAT 3558	QY	379 ATGGTACCGAAGGGCTACCGAGTGCCATTACGGCGTACCTGGCTGAAGGCTGTCCGC 438
y	3301 ATCATCGAGGCTATGAAGATGGAAAGCAAAATCACTGGCTTCGGTGAACGGCAAATGGAT 3360	Db	181 ATGGTACCGAAGGGCTACCGAGTGCCATTACGGCGTACCTGGCTGAAGGCTGTCCGC 240
b	3559 CGCGTTGGTCCGCTGGCAACGAAGGTGGAAAGGTGGGACTTGAGTCGGTCTCGTT 3618	QY	499 CGGCTTGGCTGGGAAACGGCATTACTTTGGCCAAACCCAGAGGT 558
y	3361 CGCGTTGGTCCGCTGGCAACGAAGGTGGGACTTGAGTCGGTCTCGTT 3420	Db	301 CGAGCTTGGCCGGAGTGGCTGAAGGCTTAAAGGGCATTACTTTGGCCAAACCCAGAGGT 360
y	559 CTGATCTACCGGTGATAAGTCGGGGTAAACGGCGGCTGGCTGGCTGGCCA 618	RESULT 11	QY
b	361 CTGATCTACCGGTGATAAGTCGGGGTAAACGGCGGCTGGCTGGCCA 420	DEFINITION Novel polynucleotide	Db
y	619 GTTTGGGAAATCCACCCGAGCAAAACATCGATGAGATCGTTAAAGGGCTGAAGGC 678	ACCESSION BD162966	QY

541	CCCATCTTGTAAAGGCAGTTGCCGTTGGGGACCCGGTATGGCTTTCCTCA	600
748	CCTGATGAGCTTGCCTAACAGAACGCACTCGTGAAGCTGAAGGGCTTTCGGC	807
601	CCTGATGAGCTCGCAAATTGGCAACAGAACGCACTCGTGAAGCTGAAGGGCTTTCGGC	660
808	GATGGCGGGTATATGTCGAACGGTCTGTGATTAACCCCTCAGGATATTGAAGTGCAGATC	867
661	GACGGTTCGGTATATGTCGAACGGTCTGTGATTAACCCAGCACATTGAAGTGCAGATC	720
868	CTTGGCGATCACACTGGAGAAGTTGTACACCTTTATGAACAGTGAATGCTCACTGCAGCGT	927
721	CTTGGCGATCGCACTGGAGAAGTTGTACACCTTTATGAACAGTGAATGCTCACTGCAGCGT	780
928	CGTCACCAAAAGTGTGAAATTGGCCACAGCATTGGATCCAGAACCTGGTGTGAT	987
721	CGTCACCAAAAGTGTGAAATTGGCCACAGCATTGGATCCAGAACCTGGTGTGAT	840
988	CGCATTTGTGGGATGGCAGTAAAGTCTGGCCAGCACGGCATTGGATCCAGGGGGAAACC	1047
841	CGCATTTGTGGGATGGCAGTAAAGTCTGGCCAGCACGGCATTGGATCCAGGGGGAAACC	900
1048	GTGGAATTCTTGTGAAAGGGCAACCAACAGTCTTCATCGAAATGAACCCACGTATC	1107
901	GTGGAATTCTTGTGAAAGGGCAACCAACAGTCTTCATCGAAATGAACCCACGTATC	960
1108	CAGGTGAGCACACCGAACCCAGTGAAGTCAACGGGAGCTGGGACCTGGGAGATG	1167
961	CAGGTGAGCACACCGAACCCAGTGAAGTCAACGGGAGCTGGGACCTGGGAGATG	1020
1168	CGCTTGGCTGCTGGCAACCTTGAGGAATGGGTCTGACCCAAAGATAAGATCAAGACC	1227
1021	CGCTTGGCTGCTGGCAACCTTGAGGAATGGGTCTGACCCAAAGATAAGATCAAGACC	1080
1228	CACGGTGCAGGCACTGGCAACCTTGAGGAATGGGTCTGACCCAAAGATAAGATCAAGACC	1287
1081	CACGGTGCAGGCACTGGCAACCTTGAGGAATGGGTCTGACCCAAAGATAAGATCAAGACC	1140
1288	GATACCGGAAACTATCACCGGCTACCGGCTCACCAAGGGCTTCCGCCA	1140
1141	GATACCGGAAACTATCACCGGCTACCGGCTCACCAAGGGCTTCCGCCA	1140
1348	GCAGCTCAGCTGGGAAATCACCGGCTACCGGCTCACCAAGGGCTTCCGCCA	1347
1201	GCAGCTCAGCTGGGAAATCACCGGCTACCGGCTCACCAAGGGCTTCCGCCA	1260
1408	TGCCGTGGTCCGACTGGCAGTGGCAACCTTGAGGTGGCTTGAGTTTC	1467
1261	TGCCGTGGTCCGACTGGCAGTGGCAACCTTGAGGTGGCTTGAGTTTC	1320
1468	ACCGTGTCTGGTGAACCAACATTGGTTCCTGGCTGGCTGGGAGAGGAC	1527
1321	ACCGTGTCTGGTGAACCAACATTGGTTCCTGGCTGGGAGAGGAC	1380
1528	TTCACCTCCAAGGGCATGCCAACCGGATTCACTGCCGACCTCCTTCAGGGCT	1587
1381	TTCACCTCCAAGGGCATGCCAACCGGATTCACTGCCGACCTCCTTCAGGGCT	1440
1588	CCACCTGCTGTGATGAGCAAGGGGAGCTGGCAGATGTCAACCGTGAAC	1647
1441	CCACCTGCGGATGAGCAAGGGGAGCTGGCAGATGTCAACCGTGAAC	1500
1648	AAGCCTCATGGTGTGCCACTGGCAAGGGTCAAGCTCTGCTAACATC	1707
1501	AAGCCTCATGGTGTGCCACTGGCAAGGGTCAAGCTCTGCTAACATC	1560
1708	TTTGTGCTCGTCACTGCCAACGGCTTCCGGTCAAGGGACTGGCAGCTGGCAGC	1767
1561	TTTGTGCTCGTCACTGCCAACGGCTTCCGGTCAAGGGACTGGCAGCTGGCAGC	1620
1768	TTTGTGCTCGTCACTGCCAACGGCTTCCGGTCAAGGGACTGGCAGCTGGCAGC	1827
1621	TTTGTGCTCGTCACTGCCAACGGCTTCCGGTCAAGGGACTGGCAGCTGGCAGC	1680
QY	GCACCCAGTCTTGTGCTGCCAACGGCTTCCGGTCAATTGGCACTGAGGCTTGGGGAGAG	1887
Db	GCACCCAGTCTTGTGCTGCCAACGGCTTCCGGTCAATTGGCACTGAGGCTTGGGGAGAG	1740
QY	GCGCTGCAAAGCTGACTCCTGAGCTTTGTGCTGCCAACGGCTTCCGGTCAATTGGCACTGAGGCTTGGGGAGAG	1947
Db	GCGCTGCAAAGCTGACTCCTGAGCTTTGTGCTGCCAACGGCTTCCGGTCAATTGGCACTGAGGCTTGGGGAGAG	1741
QY	GATGTGGCGATGGCTTCCCTTGTGATCCGGGCTGGGACAGGGCTGCGCGAG	2007
Db	GATGTGGCGATGGCTTCCCTTGTGATCCGGGCTGGGACAGGGCTGCGCGAG	1860
QY	GCGATGCCAGTAAACATTCAAGTGCCTGGCTGGGAAACACCGTGGGATAACACC	2067
Db	GCGATGCCAGTAAACATTCAAGTGCCTGGCTGGGAAACACCGTGGGATAACACC	1920
QY	CCGATGCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	2127
Db	CCGATGCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	2068
QY	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	2187
Db	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	1861
QY	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	2008
Db	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	1980
QY	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	2068
Db	CGTACCCAGACTCCGCTCTGCCGCTTCCAGGCTCCGGGGGGAC	1921
QY	ATCTTCCGCACTTTCGACGGCCTTAACCGACGTCCTCCAGCAATCGACGCA	2187
Db	ATCTTCCGCACTTTCGACGGCCTTAACCGACGTCCTCCAGCAATCGACGCA	2128
QY	GTCCTGGGAGACCAACACCGGCTAGCCCAGGGTAGGGCTATGGCTTATTCTGGTATCTCTCT	2247
Db	GTCCTGGGAGACCAACACCGGCTAGCCCAGGGTAGGGCTATGGCTTATTCTGGTATCTCTCT	21981
QY	GATCCAAATGAAAAGCTCTACACCCCTGAGTAAAGATGGCAGAGGATCGTC	2307
Db	GATCCAAATGAAAAGCTCTACACCCCTGAGTAAAGATGGCAGAGGATCGTC	2041
QY	2248 GATCCAAATGAAAAGCTCTACACCCCTGAGTAAAGATGGCAGAGGATCGTC	2308
Db	2248 GATCCAAATGAAAAGCTCTACACCCCTGAGTAAAGATGGCAGAGGATCGTC	2101
QY	2308 AGTCTGGCGCTCACATCTGGCCTAACATCGATCTGCCAGCTGGG	2367
Db	2308 AGTCTGGCGCTCACATCTGGCCTAACATCGATCTGCCAGCTGGG	2161
QY	GTAACCAAGCTGGCTCACCATCTGGCCTAACATCGATCTGCCAGCTGGG	2368
Db	GTAACCAAGCTGGCTCACCATCTGGCCTAACATCGATCTGCCAGCTGGG	2221
QY	2428 CACGACACTGGGGTGGCTCGGCCAACCTGCTGAGCTCAAGCTGGGAGAT	2487
Db	2428 CACGACACTGGGGTGGCTCGGCCAACCTGCTGAGCTCAAGCTGGGAGAT	2280
QY	2488 GCTGTTGACGGTGCATTGGCAACCCGGTGGCTGAGCTGGCCTGAGCACC	2427
Db	2488 GCTGTTGACGGTGCATTGGCAACCCGGTGGCTGAGCTGGCCTGAGCACC	2340
QY	2548 ATTGTTGCTGTCATTGGCTCACATCTGGCCTAACATCGATCTGCC	2547
Db	2548 ATTGTTGCTGTCATTGGCTCACATCTGGCCTAACATCGATCTGCC	2341
QY	2608 GACCTCGAGCCGCTTCCGCCATCCCTGCTGGCTGAGCTGGGAGAT	2607
Db	2608 GACCTCGAGCCGCTTCCGCCATCCCTGCTGGCTGAGCTGGGAGAT	2460
QY	2461 GACCTCGAGCCGCTTCCGCCATCCCTGCTGGCTGAGCTGGGAGAT	2667
Db	2461 GACCTCGAGCCGCTTCCGCCATCCCTGCTGGCTGAGCTGGGAGAT	2520
QY	2668 CCAGGCCAACCGGTGGCTGAGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2727
Db	2668 CCAGGCCAACCGGTGGCTGAGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2721
QY	2728 CGTGCACAGGCCAACCGGTGGCTGAGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2787
Db	2728 CGTGCACAGGCCAACCGGTGGCTGAGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2581
QY	2788 GCGGACCTCCGCACTGGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2847
Db	2788 GCGGACCTCCGCACTGGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2700
QY	2848 GGCGACCTCCGCACTGGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2760
Db	2848 GGCGACCTCCGCACTGGCTGGGAGACTGTACCTGCCATTCTGAAACTAC	2701

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 3427; Conservative 0;

QY 2908 CCACAAAAGTACGACAATCCCAGACTCTCATCGCGTTCCCTGCCGGAGGTTGGTAAC 2967
Db 2761 CCACAAAAGTACGACAATCCCAGACTCTGTCACTCGCGTTCCCTGCCGGAGGTTGGTAAC 2820

QY 2968 CTCAGGTRGGCTGGCAGAGCCAACTTGCGAACCCGGCAACTGGAAAGGCC 3027
Db 2821 CTCAGGTRGGCTGGCAGAAACCCTGCGAACCCGGCAACTGGAAAGGCC 2880

QY 3028 AAGGCACCTCTGACGAAAGTCCGTGAGGAAGGGCAACCTCGACGCTGATGATTCC 3087
Db 2881 AAGGCACCTCTGACGAAAGTCCGTGAGGAAGGGCAACCTCGACGCTGATGATTCC 2940

QY 3088 AAGGAACCTCGCAAAAGCCTCAACCGCTGCTGTTCCCGAAGGCAACCGAAGGTTCTC 3147
Db 2941 AAGGAACCTCGCAAAAGCCTCAACCGCTGCTGTTCCCGAAGGCAACCGAAGGTTCTC 3000

QY 3148 GAGCACCGTGCCTCGGAAACACCTCTGGATGATGTTACGGC 3207
Db 3001 GAGCACCGTGCCTCGGCAACACCTCTGGCTGGATGATGTTACGGGA 3060

QY 3208 CTGGTCGAAGGCCGAGACTTTGATCCGCTGCCAGATGTGCGCACCCCCACTGCTTGT 3267
Db 3061 CTGGTCGAAGGCCGAGACTTTGATCCGCTGCCAGATGTGCGCACCCCCACTGCTTGT 3120

QY 3268 GCCTGGATGGGATCTGCAAGCAGATAAGGGTATGCAATGGGCAACGTC 3327
Db 3121 GCCTGGATGGGATCTGCAAGCAGATAAGGGTATGCAATGGGCAACGTC 3180

QY 3328 AACGGCCAGATCCGCCAATGGGTGCGTGAACGGCTCCTGACCCGCAACC 3387
Db 3181 AACGGCCAGATCCGCCAATGGGTGCGTGAACGGCTCCTGACCCGCAACC 3240

QY 3388 CGAGAAAAGGCCAGATTCCTCCAAACAAAGGCCATGGCTGGGACCATTCGCTGGTGTG 3447
Db 3241 CGAGAAAAGGCCAGATTCTCCAAACAAAGGCCATGGCTGGGACCATTCGCTGGTGTG 3300

QY 3448 ACCGTTGACTGTTGCTGAAGGTGAGGTCAAGGCTGGAGATCGTCAATCGAG 3507
Db 3301 ACTGTTGACTGTTGCTGAAGGTGAGGTCAAGGCTGGAGATCGTCAATCGAG 3360

QY 3508 GCTATGAAAGTGGAAAGCRAACAATCACTGCTTCTGTGACGGCAAATCGTGGTGTG 3567
Db 3361 GCTATGAAAGTGGAAAGCRAACAATCACTGCTTCTGTGACGGCAAATCGTGGTGTG 3420

QY 3568 GTTCCCTGCTGCAACGAAAGTGGAAAGGTGGCAACTTGATGCTGTTCTAA 3621
Db 3421 GTTCCCTGCTGCAACGAAAGTGGAAAGGTGGCAACTTGATGCTGTTCTAA 3474

RESULT 13
AX453603 LOCUS AX453603 DNA linear PAT 06-JUL-2002
DEFINITION Sequence 3 from Patent WO200231158.
VERSION AX453603 GI:21712843
KEYWORDS Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteraceae; Corynebacterium.
REFERENCE 1. Hanke, P.D.
AUTHORS Feedback-resistant pyruvate carboxylase gene from corynebacterium
TITLE /organism="Corynebacterium glutamicum"
JOURNAL /mol_type="unassigned DNA"
FEATURES /db_xref="taxon:1718"
Source Location/Qualifiers
1. .3474
/db 1108 1048 901 961 1168
Patent: WO 0231158-A 3 18-APR-2002;
ARCHER-DANIELS-MIDLAND COMPANY (US)
Query Match Score 3398.8; DB 6; Length 3474;

Db	1021	CGCTTGGCTGGTGCACCTTGAAAGGAAATTGGGTGACCCAAAGATAAAGATCAAGACC	1080	Qy	2308	AAGTCTGGCCCTCACATCTGGCCATTAAAGGATAATGGCTGGTCTGCTGCCAGCTGCC	2367
Qy	1228	CACGGTGGCAGCACTGCACTGGCGATCACCAACGGAAAGATCCAACAAACGGCTTCGGCCA	1287	Db	2161	AAGTCTGGCCCTCACATCTGGCCATTAAAGGATAATGGCTGGTCTGCTGCCAGCTGCC	2220
Db	1081	CACGGTGGCAGCACTGCACTGGCGATCACCAACGGAAAGATCCAACAAACGGCTTCGGCCA	1140	Qy	2368	GTAACCAAGCTGGTCAACGGCAACTGGGCCATTGGCTGAATTGCACTGCAAGTCAACACC	2427
Qy	1288	GATAACCGGAACTATACCGGTACCGGCTCACCGGCTCACCGGCTCACCGGCTCACCGG	1347	Db	2221	GTAACCAAGCTGGTCAACGGCAACTGGGCCATTGGCTGAATTGCACTGCAAGTCAACACC	2280
Db	1141	GATAACCGGAACTATACCGGTACCGGCTCACCGGCTCACCGGCTCACCGGCTCACCGG	1200	Qy	2428	CAGGACACTGGGGTGGCAGGCTGGCAACCTTGGCTGAAGGCTCAAGGCTGGTCAAGGAT	2487
Qy	1348	GGAGCTCAAGCTGGTGGCGAAATCACCGAACACCTTGTACTCCATGTTGGTGAATGACC	1407	Db	2281	CAGGACACTGGGGTGGCAGGCTGGTCAAGGCTCAAGGCTGGTCAAGGAT	2340
Db	1201	GGAGCTCAAGCTGGTGGCGAAATCACCGAACACCTTGTACTCCATGTTGGTGAATGACC	1260	Qy	2488	GCTGGTGAACGGGTGCTTCCGACCACTCCAGGCCATCCCTGCTTGCC	2547
Db	1261	TGCGTGGTTCCGACTTTGAACACTGCTGTTGACACGGGCGTGGCTGAGTTC	1467	Db	2341	GCTGGTGAACGGGTGCTTCCGACCACTGCTGGTCAAGGCAACCTCCAGGCCATCCCTG	2400
Qy	1408	TGCCGTGGTTCCGACTTTGAACACTGCTGTTGACACGGGCGTGGCTGAGTTC	1467	Qy	2548	ATTGGTGGCTGCAATTGGGCAACCCGGTGGGATACGGGTTGAGGCTGGTTCTGAGGCTGG	2607
Db	1321	ACCGTGTCTGGTGTGGTGGCAACCAACATTGGTTCTGGTGGCTGGGGAGGGAC	1527	Db	2401	ATTGGTGGCTGCAATTGGGCAACCCGGTGGGATACGGGTTGAGGCTGGTTCTGAGGCTGG	2460
Db	1321	ACCGTGTCTGGTGTGGTGGCAACCAACATTGGTTCTGGTGGCTGGGGAGGGAC	1380	Qy	2608	GACTCTGAGGCCGTACTGGGAAGGAGCTGGGGACTGTGACCTGCCATTGAGTCTGGAACC	2667
Qy	1528	TTCACCTTCAAGCGGATGCCAACCGGATTCATTGGGATCACCCGACCCGGATCACCG	1587	Db	2461	GACTCTGAGGCCGTACTGGGAAGGAGCTGGGGACTGTGACCTGCCATTGAGTCTGGAACC	2520
Db	1381	TTCACCTTCAAGCGGATGCCAACCGGATTTATGGGATCACCCACCCACCC	1440	Qy	2668	CCAGGGCCCAAACGGGTGGCTAACGCCAACAAATCCAGGGACAGTGTGCCAACCTG	2727
Qy	1588	CCACCTGTGTGTATGATGATGAGCAGGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC	1647	Db	2521	CCAGGGCCCAAACGGGTGGCTAACGCCAACAAATCCAGGGACAGTGTGCCAACCTG	2580
Db	1441	CCACCTGGGGATGATGAGCAGGGGACGCATCCTGGATTACTTGGCAGATGTCACCGTGAAC	1500	Qy	2728	CGTGGCACAGGGCCACCGGCACTGGGCCCTTGGGATCGTTGAGCTCATGGAAGACAATAC	2787
Qy	1648	AAGCCTCATGGTGTGCGTCCAAGGATGTTGAGCTAACATC	1707	Db	2581	CGTGGCACAGGGCCACCGGCACTGGGCCCTTGGGATCGTTGAGCTCATGGAAGACAATAC	2640
Db	1501	AAGCCTCATGGTGTGCGTCCAAGGATGTTGAGCACAATGATAAGGTGCCAACATC	1560	Qy	2788	GCAGCCGTTAATGAGATGCTGGGACGCCAACCAAAGGTCAACCCCACCTCCAAAGGGTGT	2847
Qy	1708	AAGGATCTGCCACTGCCAACGGGCTCCGTGAGCCGCTGGCCAGCCGGG	1767	Db	2641	GCAGCCGTTAATGAGATGCTGGGACGCCAACCAAAGGTCAACCCCACCTCCAAAGGGTGT	2700
Db	1561	AAGGATCTGCCACTGCCAACGGGCTCCGTGAGCCGCTGGCCAGCCGG	1620	Qy	2848	GGGACACTCCACCTCGGCACTCCAGACATCCAGGCTGGTCACTCGGTCTGCTGCCGAT	2907
Qy	1768	TTTGCTCGTGTACTCTCGTGTAGCAGGAGCCACTGGCACTGGCTTACTGATAACCTTCCGGAT	1827	Db	2701	GGGACACTCCACCTCGACTCCAGACATCCAGGCTGGTCACTCGGTCTGCTGCCGAT	2760
Db	1621	TTTGCTCGTGTACTCTCGTGTAGCAGGAGCCACTGGCTTACTGATAACCTTCCGGAT	1680	Qy	2908	CCACAAAGTAGACGACATCCAGACTCTGTCATCGGTCTCTGCTGCCAGGCTGGTAAC	2967
Qy	1828	GCACACCAAGCTGACTCTCGTGTAGCAGGAGCCACTGGCACTGGCTGGGCCAGAC	1887	Db	2761	CCACAAAGTAGACGACATCCAGACTCTGTCATCGGTCTCTGCTGCCAGAAGCTGGTGT	2820
Db	1681	GCACACCAAGCTGACTCTCGTGTAGCAGGAGCCACTGGCTTACTGATAACCTTCCGGAT	1740	Qy	2968	CCTCCAGGTGGCTGGCCAGGCACTGGCACTGGCTGGCCAGGCTGGCTGGCCAGG	3027
Db	1741	GCACACCAAGCTGACTCTCGTGTAGCAGGAGCCACTGGCTTACTGATAACCTTCCGGAT	1800	Db	2821	CCTCCAGGTGGCTGGCCAGAACCCAGACTCTGTCATCGGTCTCTGCTGCCAGG	2880
Qy	1948	GATGTCGGGATGCTGCTTCCGTGAGCTTCCGTGAGGATCCCTGGGAGCTGGCAG	2007	Qy	3028	AAGGCACACTCTGACGGAAAGTTCTGAGGAAGGAGCAGGGCACCTCGACGGTGTGATGATTCC	3087
Db	1801	GATGTCGGGATGCTTCCGTGAGCTTCCGTGAGGATCCCTGGGAGCTGGCAG	1860	Db	2881	AAGGCACACTCTGACGGAAAGTTCTGAGGAAGGAGCAGGGCACCTGGTGTGATGATTCC	2940
Db	1741	GCGATGCCGAATGTAACATTCAAGTCAAGTCAAGTCAAGTCAAGTCAACCC	1920	Qy	3088	AAGGAACACTGCCAAATAGCTCAACCCGCTCAACCGCAACCCGAAAGGTCCTC	3147
Qy	2008	GCGATGCCGAATGTAACATTCAAGTCAAGTCAAGTCAAGTCAAGTCAACCC	2067	Db	2941	AAGGAACACTCTGACGGAAAGTTCTGAGGAAGGAGCTGGCTGGTGTGATGATTCC	3000
Db	1861	GCGATGCCGAATGTAACATTCAAGTCAAGTCAAGTCAAGTCAACCC	1920	Qy	3148	GAGCACCGTGGCCAAACACCTCTGCGCTGGATGTCGAAATTCTCTACGGC	3207
Qy	2068	CCGATGCCGAATGTAACATTCAAGTCAAGTCAAGTCAAGTCAAGTCAACCC	2127	Db	3001	GAGCACCGTGGCCAAACACCTCTGCGCTGGATGTCGAAATTCTCTACGGC	3060
Db	1921	CCGATGCCGAATGTAACATTCAAGTCAAGTCAAGTCAAGTCAACCC	1980	Qy	3208	CTGTCGAAGGGCCGAGACTTCTGGCCCTGCGAGCTGGCTGGTGTGATCTCT	3267
Qy	2128	ATCTTCCGCACTTGTGACCGGCTTAACGACGTTCCCAAGATGGCTCCAGCAATCGACGCA	2187	Db	3061	CTGTCGAAGGGATCTGTCAGGCAACCCACTGCTGGTGTGATCTCTACGGC	3120
Db	1981	ATCTTCCGCACTTGTGACCGGCTTAACGACGTTCCCAAGATGGCTCCAGCAATCGACGCA	2040	Qy	3268	CGCTGGATGGGATCTGAGGCAAGGATAAGGTATGGCAATGTTGTCACGCCAAC	3327
Qy	2188	GTCCTGGAGACCAACACCGGGTAGCCGGACTGGCTGGCTGACCGCTCCGGTGA	2247	Db	3121	CGCTGGATGGGATCTGTCAGGCAACCCACTGCTGGTGTGATCTCTACGGC	3180
Db	2041	GTCCTGGAGACCAACACCGGGTAGCCGGACTGGCTGGCTGACCGCTCCGGTGA	2100	Qy	3328	AACGCCAGATCCGCCAATGGCTGGCTGACCGCTCCGGTGAAGTGTCAACGCCAAC	3387
Qy	2248	GATCCAATGAAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGGAGATCGTC	2307	Db	3181	AACGCCAGATCCGCCAATGGCTGGCTGACCGCTCCGGTGAAGTGTCAACGCCAAC	3240
Db	2101	GATCCAATGAAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGGAGATCGTC	2160				

RESULT 14

AP005216 LOCUS AP005216 308750 bp DNA linear BCT 10-JUL-2003 DEFINITION Corynebacterium efficiens YS-314 DNA, complete genome, section 3/11.

ACCESSION AP005216 BA000035 VERSION AP005216.1 GI:23492422

KEYWORDS Corynebacterium efficiens YS-314

ORGANISM Corynebacterium efficiens YS-314

BACTERIA; Actinobacteria; Actinomycetales; Corynebacteriaceae; Corynebacterium.

REFERENCE 1 Nishio, Y., Nakamura, Y., Kawarabayasi, Y., Usuda, Y., Kimura, E., Sugimoto, S., Matsui, K., Yamagishi, A., Kikuchi, H., Ikeo, K. and Gojobori, T. Comparative Complete Genome Sequence Analysis of the Amino Acid Replacements Responsible for the Thermostability of Corynebacterium efficiens Genomic Res. 13 (7), 1572-1579 (2003)

JOURNAL 22723752

MEDLINE 12840036

PUBMED 2 (bases 1 to 308750)

REFERENCE 2 Kawarabayasi, Y., Yamazaki, J., Hino, Y., Kikuchi, H. and Director-General of Biotechnology Center.

AUTHORS Submitted (17-MAY-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibusawa-ku, Tokyo 151-0066, Japan (E-mail: bio@nite.go.jp, Tel: 81-3-3481-1933, Fax: 81-3-3481-8424)

TITLE Kawarabayasi, Y. is officially affiliated with the National Institute of Advanced Industrial Science and Technology, Tsukuba, Ibaraki, 305-8566 Japan

COMMENT Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan Itoh, T. is at the Japan Biological Information Research Center, Koto-ku, Tokyo, 135-0064 Japan

Yamagishi, A. is at Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo, 192-0392 Japan

Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co., Inc., Kawasaki, Kanagawa, 210-8681 Japan

The other authors are at the National Institute of Technology and Evaluation, Shibusawa-ku, Tokyo, 151-0066 Japan.

FEATURES Source

1. 308750 /organism="Corynebacterium efficiens YS-314"

/mol_type="genomic DNA"

/strain="YS-314"

/db_xref="taxon:196164"

155. .598 /note="CE0586, similar to AE007159-8|AAK47889.1| percent

/codon_start=1

/transl_table=11

/product="putative 50S ribosomal protein L13"

/protein_id="BAC17396.1"

CDS

Qy 3388 GCAGAAAAGGAGATTCCCAAACAAGGCCATGGTGTGCCACCATCGCTGGTTGTC 3447 /db_xref="GI:23492423" /translation="MSTYHPKSGDITRKRWYVIDATDVVLGRILATHAADLRLGKGKPLF APNVDGDRVIIINADKVITSNKRDEMRYRHSGYPGLKSMTLGRSLLEHPERVLE ESIIGMMPHNKLTAASVKKLHVFGSEHPYAAQKPETYEIKKVAQ" 598. .1146 /note="CE0587, similar to AL583918-48|CAC29873.1| percent identity: 59 in 159 aa" /codon_start=1 /transl_table=11 /product="putative 30S ribosomal protein S9" /protein_id="BAC17397.1"

Db 3301 ACTGTGACTGTTGCTGAAGGTGATGGTCAAGGCTGAGATCCATCGCAATCATCGAG 3507 /db_xref="GI:23492424"

Qy 3508 GCTATGAAATGGAACAAATCACTGCTTCTGTTGAGGGCAAAATCGATCGCTTGTG 3567 /translation="MSEPIQENVESNVADAADIATAATAEEFTNTIGDAISTSTTEE ETPEAAAPAVLDGPPIWTVGRKRAIVVRVMVAGSGEITCNGRTILEDYFPNLKHQOLIKA PLVLLGREGQFDIHANLGGGPTQAGAFAFRILAIARALNAYNAERPTLKAGPLTRDA RAVERKTAGLHKARRAPQYSKR" 1282. .2670 /note="CE0588, similar to AL031317-14|CAA20392.1| percent identity: 62 in 448 aa" /codon_start=1 /transl_table=11 /product="putative phospho-sugar mutase" /protein_id="BAC17398.1"

Db 3361 GCTATGAAATGGAACAAATCACTGCTTCTGTTGAGGGCAAAATCGATCGCTTGTG 3420 /db_xref="GI:23492425"

Qy 3568 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3621 /translation="AHVLTAGTRPHGRPPVAIVGRDPRVSGEMLAALAAGMASRGVDVLRGVVIPTPGVA FLTDGYGADMGMISASHNPMPDNGIKFFSAGGHHKLPEDEVDEIERVMDLPPEEGPTG HGIGRIVTEAAPDARGRGLYQLQHLADAVPTDLSGITVYVDAANGAASVIAPOAYEAAGAKV IAIHNTPNAYNINERCGGSTHMDOQAOAVLEHGAHDGDCLAVDSDGNIVDG DQIMALLAIAMKENSELRLNTLVATVMNGLKLMAMEKADIQLRTTQVAMTFLPQVLI AGGFALGGEQSGHIVLPDQHGTGDTGTLGTSILMARMAATGKPELSELPRVMVEAAEQQARR NVPVADKSSIMKSANTQAAVAAEEELGGTGRVLLRPSGTEELPRVMVEAAEQQARR VAGRILAAVVAEA"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0589" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17399.1"

CDS

2742. .3071 /note="CE0589" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17399.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0589" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17399.1"

CDS

2742. .3071 /note="CE0589" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17399.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0589" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17399.1"

CDS

3068. .4462 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

CDS

3068. .4462 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

CDS

3068. .4462 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

CDS

3068. .4462 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

Db 3421 GTTCCCTGCTGCAACGAACGGTGGCAAGTGGCCACTTGATGTCGTTCTCTAA 3474 /note="CE0590" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC17400.1"

CDS

```

<product>="conserved hypothetical protein"
<protein id="BAC17402.1">
<db xref="GI:23492429">
</db>
<translation>"MAHPGRIILPSGVTLSTILDRAENLKKHLSKLSKRGPFRVMVG
DLDYAGLPGKLYTPTAEGNGVPGVAEFGHDWMEKTHQTLRHLASWGLIAAVAAAPNTETG
ELPDDEHRGEAADLDSALQIILLAGVKLGAGKVTVNPGGLGLVGHGMGGGTVAVLAAANRKAV
RAVGALYPASTSFSVCDAAPAVKAPEGLIIGTADLGMFDAGDPAKVAARWGGDVYREL
DNGNQQGFSEDTMPKLLVGVGRPQTAGQBLARGLLTGFLILHOLAGERSYKAFSDPEAE
AKKVTTSYWGIDEEKAFQODESPLPFLNSN"
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 7 GGGGTTAGATCTGGGGGGTTATTCACTTGGCTTGAAGTCGTGCAGGTCAAGGG 66
Db 128583 GGGGTCCTGGGGGCACTTTCACGGCAAGGTGGTGAATTCCGCAGTCACTC 128642
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 67 GAGGGTTGCCGAAACATTGAGAGAAAACAAAACCGATGTTGATGGGGAAATCGG 126
Db 128643 CCCGGCGGGGTAGAGAACGGGAAAGCAATACGTGGTTTTCGGACTGG 128702
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 127 GGGTTACGATACTAGGACCGAGTGAATCACCTTCAACGCTTCCAGCATC 184
Db 128703 CCGTTACGATGTTCTGAAG-AGTGACTGCCATACCCAAACAGGCTTAC 128761
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 185 GAATAATTACTCTAGTGTGACTCACACATCTTCAACGCTTCCAGCATC 244
Db 128762 GAAACAAAATCTGGTTACAACA--ACACCCCTCAAGGCTC 128818
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 245 TGGTAGCAAACCGGGGAATCGCGTCCCGTGTCCGGACTCGAACCGGGTG 304
Db 128819 TGGTGGCCAACGGAGGTGAATCGGGGTGGAGCATCGGGGGGG 128878
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 305 CAGCCACGGTAGCTTACCCCGTGAAGATCGGGATCATTCACCGCTCTTGCTT 364
Db 128879 CCGCAACCGTGGCCATCTACCCCGGGACCGTGGCTCTTGCTT 128938
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 365 CTGAAGCTGTCCGATTGGTACCGAGGCTCACAGCTAACCGGATCATCGATG 424
Db 128939 CCGAGGGGTGAGGATCGAACGAGGGCTCACCGTCAAGGGCTTACCTCGAT 128998
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 425 AAATTATCGGTGAGCTAACCGGATTACCTTTATGGCTTACGGCTTCC 484
Db 128999 AGATCATCAACGGGCCAGAACGGTGAAGGGCTTACCGGGCTATGGTTCC 129058
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 485 TGTCTGAATANTGCCAGCTTGCAGTGTGGAAAACGGCATTACTTTATGGCC 544
Db 129059 TTTCGGAAAATGCCAGCTCGACCTCACGGGACAAGTCCAAGGGCTTACCTCTCATGGTC 129118
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 545 CAACCCAGAGGGTTCTGATCTCACCGGTGATAAGCTCCGGGAAATCCACCCGAGGAATCCACCCCAAGGGAAATCCACCCAGGCTGGCTGGCTGGTCA 129178
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 605 AGGTGGTCTGCCAGTTGGGAATCCACCCGAGGAATCCACCCAGGCTGGCTGGCTGGTCA 129238
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 665 AAAGGCTGAAAGCCAGACTTACCCCATCTTGTGAAGGGCAATTGGCTGGGGAC 724
Db 129239 AGAGTGGCGAGGGCAACCTACCCGATCTTGTCAAGGGCTGGGGGG 129298
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 725 GCGGTATGGGGTTTCGGCTTCACTGTGATGAGCTTGGCAAAATTAGCAAGGCTCTC 784
Db 129299 GTGGTATGGGGTTTCGGCTTCACTGTGATGAGCTTGGCAAAATTAGCAAGGCTCTC 129358
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 785 GTGAAGCTGAAGGGCTTTCGGGATGGCGGATAGTGTGAAACGTCCTGTGATTAACC 844
Db 129359 CGAGGGGAGGGCGCTTCGGTGAAGGGATCCGTCAAGTGTGAAACGGGCCGTGATCAAAC 129418
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 845 CTAGGATATTGAAGTGCAGATCACACTGGAGAAAGTTGTCGAAATTGGCCAGCACGC 904
Db 129419 CCCAGCACATCGAGGTGAGATCCCTGGTGAACACGGCGATGTCACTCCACCTGTATG 129478
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 905 AACGTGACTGCTCACTGCAAGGGTCTGGCTCGTCGAAATTGGCCAGCACGC 964
Db 129479 AACGGGACTGTTCCCTGAGGGCCACCAAGGGTCTGGGAGATCGCACCTGCCCAGC 129538
```

gene 5737 . 6840 Query Match 63 . 0% ; Score 2282 . 8 ; DB 1 ; Length 308750 ;
 /gene="a1r" Best Local Similarity 77 . 7% ; Pred. No. 0 ; Mismatches 0 ; Matches 2810 ; Conservative 4 ; Gaps 4 ;

```

Qy 965 ATTGGATCCAGAACCTGCGGTGATGCAAGTAAAGTTCGCGCTCCA 1024
Db 129539 ACCTCGAACCGGAGCTGGCGATCTGTGAACTCCAAATCCA 129598
```


Db		131756	ATGACCGCGAGTTCTCTACGGCTTGAAGGAGGACGTGAGGGACTGATCCGACTGACCG	131815	/organism="Corynebacterium thermoaminogenes"
QY	3245	ATGTGCGAACCCCACTGCTGGATGGATCTCTGAGCTGGATGGGGTAAAGGGTA	3304	/mol_type="genomic DNA"	
DB	131816	GTGTGCTAACCCGATGGTGGTGGCTGGATGGGGTAAAGGGTA	131875	/db_xref="taxon:161484"	
QY	3305	TGGCAATGGTGGCCAACGGCAATGCCCAATGGGTGGTGGGGTAAAGGGTA	3364	ORIGIN	
DB	131876	TGGCAACGGTGGTCAACGTGTCAGGGCAATGGGGTAAAGGGTA	131935	Query Match 63.0%; Score 2279.6; DB 6; Length 4013;	
QY	3365	CCGGTGGAGTCCGTACCGGCCAACCGCAGATTCCTCAAACAGGGCCATGTTG	3424	Best Local Similarity 77.7%; Pred. No. 0;	
DB	131936	CCGGTGGAGTCCGTACCGGCCAACGGGGATGCCACAAAGGGCATGTCG	131995	Mismatches 0; Conservative 0; Indels 9; Gaps 4;	
QY	3425	CTGGCACATTGCTGGTCAACCGCAGAAAAGGGAGATGGTCAAGGCTG	3484	Matches 2808; Conservatve 7	
DB	131996	GCGCACATTGCCGTACCGGCCAACGGGGATGCCACAAAGGGCATGTCG	132055	GGGGTTAGATCCTGGGGTTATTCACTTGCAGTTGGCTGAAGTCAGGTCAGGG	
QY	3485	GAGATGGCAGTGGCAATTATCGAGGGCTATGAAGATGGAAACAATCA	3544	66	
DB	132056	GCGACGCCGTGGCCATCATTGAGGCCATCATGGAGGCCACCATCACGGCCCTGTG	132115	Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTCAGTGG	
QY	3545	ACGGCAAAATCGATCGGTTCTGTGCAACGGAAGGGACTGTA	3604	188	
DB	132116	ACGGTGTATCGACCGGCCACCAAGGTGAGGGTGTGAGATCAAGGCTG	132175	QY 67 GAGGTTACGATACTAGGACGCCAGTGACTGATCACCCCTTCAACGCTTCCAGCATC	
QY	3605	TGTCGTCGTTCTCA	3620	AAGAATCTGGTAAACA---ACACCTTCAACGCCAACGGTAAACAGGCTGGTCAAAAGATCC	
DB	132176	TCGGGGTCTGTCTTA	132191	307	
<hr/>		308 GAACAAAAACTGTGGTTAACACA---ACACCTTCAACGCCAACGGTAAATCGGGCTCACCGTCAAGGGTACCTGAGACCGGG			
QY	3625	TGGTAGCAAACCGGGGAATGGCTTCCGTGTGTTCCGAGCACTCGAAACCGGTG	304	424	
DB	365	GGTGGCCAACCGAGGTAAATCGGGCTGGGAAATGGCTGGGACTGAGACCGGG	424	Db 249 CGGTTAGATGTTCTGAAG-AGTGACTGCCCACACATCTAACAGATCT	
QY	365	CAGGCCACGGTGGCCATCTACCCGGGAGGACCTGGCTCCACCGTCAAGGGTACCTGAGACCGGG	364	307	
DB	425	CCGAGGGGTGAGGATCGAACGGCTAACCCGGGATCTGGCTCCCTGCCT	424	Db 127 GGGTTACGATACTAGGACGCCAGTGACTGATCACCCCTTCAACGCTTCCAGCATC	
QY	425	CTGAGCTGTCGGCATTGGTACCGAAGGCTCACAGTCAGGATCGGATCTGGCT	364	184	
DB	545	AGATCATCAACGCCCAAGGGTAAAGGGGATGGCTACCCGGGTATGGTTCC	484	Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTC	
QY	485	CCGAGGGGTGAGGATCGAACGGCTAACCCGGGAGGACCTGGCTCCCTGCCT	484	188	
DB	545	AAATTATGGTGCAGCTAAAGTTAACAGGATGGCCATTACCGGCTCTCC	484	QY 425 GAGGTTACGATACTAGGACGCCAGTGACTGATCACCCCTTCAACGCTTCCAGCATC	
QY	485	TGCTGAAAATGCCAGCTGGGGAAACGGGATTACGGCTTACCCGGATACGGCTCC	484	Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTC	
DB	605	TTTCGGAAAATGCCAGCTGGGGAAACGGCTAACCTTCATGGTC	604	Db 249 CGGTTAGATGTTCTGAAG-AGTGACTGCCCACACATCTAACAGATCT	
QY	545	CAACCCAGAGGGTCTGGTATAAGTCTCACGGGTATAAGTCTGGGATCATTCCACCGGCTAACCGCCGGAAAGA	604	307	
DB	665	CCACCCGGAGGTGCTGAACCTCACGGGAAATCCACCGGCTAACCGCCGGAAAGA	604	Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTC	
QY	605	AGGTGGTCTGGCAGTTGGGGAAATCCACCGGCTAACCGCCGGAAAGA	724	QY 425 GAGGTTACGATACTAGGACGCCAGTGACTGATCACCCCTTCAACGCTTCCAGCATC	
DB	725	AGGGCGGGCTGGGGAAATCCACCCAGCACTGGGAGGACCTGGCTGAGCTGGTCA	784	Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTC	
QY	665	AAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGGCACTGGGGGAC	724	Db 249 CGGTTAGATGTTCTGGCTAACCTGCTGGGATCTGGGCTAACAGGTC	
DB	785	AGAGTGGCGAGGGGAGCTACCCGATCTTCAGGGCTGGGGGAC	844	QY 425 GAGGTTACGATACTAGGACGCCAGTGACTGATCACCCCTTCAACGCTTCCAGCATC	
PD	12-APR-2001			Db 129 GGGGCTCGGGGATCTTTCAGGGCTGAATTCCGGTCACTTCAGGTC	
PF	04-OCT-2000	WO 20000JP006913		QY 725 GCGGTATGGCTTTGGCTCACCTGATGGCTTGGCAAAATTAGCAACAGAACATCTC	
PR	04-OCT-1999	JP 99P 282716, 01-NOV-1999	JP 99P 311147 PR	Db 845 GTGGTATGGGGCTGGCTGAGAACGCCAGGGCTCCC	
21-APR-2000	JP 00P 120687			QY 785 GTGAGGTGAGGGCTTTCGGCGATGGCGTAAAGTGTGAAAGTGTGATTAACC	
PI	SEIKO HIRANO, GEN NONAKA, YUMI MATSUZAKI, NAOKI AKIYOSHI, KANAE NAKAMURA, EIICHIRO KIMURA, TSUYOSHI OSUMI, KAZUHIKO MATSUI, YOSHIO KAWAHARA, OSAMU KURAHASHI, TSUYOSHI NAKAMATSU, SHINICHI SUGIMOTO			Db 905 GCAGGGGAGGGCGCTTCGGTGAACGGGATCCGGTCAACACAAAC	
COMMENT	OS Corynebacterium thermoaminogenes			964	
PN	WO 0125447-A/11			QY 845 CTCAGCATATTGAAAGTGAAGATCCCTGGCTGAGTACACTGGAGAAGTTGTGATACACCTTTATG	
PD	12-APR-2001			Db 905 AACGTGACTGGCTCACTGCGCTGCGGATACACTGGAGAAGTTGTGATACACCTTTATG	
PF	04-OCT-2000	WO 20000JP006913		QY 904 CTCAGCATATTGAAAGTGAAGATCCCTGGCTGAGTACACTGGAGAAGTTGTGATACACCTTTATG	
PR	04-OCT-1999	JP 99P 282716, 01-NOV-1999	JP 99P 311147 PR	Db 1024 CCAGGACATCGAGGTGAGATCCCTGGTGAACACGGGCTAACCTGTATG	
21-APR-2000	JP 00P 120687			QY 905 AACGTGACTGGCTCACTGCGCTGCGGATACACTGGAGAAGTTGTGATACACCTTTATG	
PI	SEIKO HIRANO, GEN NONAKA, YUMI MATSUZAKI, NAOKI AKIYOSHI, KANAE NAKAMURA, EIICHIRO KIMURA, TSUYOSHI OSUMI, KAZUHIKO MATSUI, YOSHIO KAWAHARA,			Db 1024 CCAGGACATCGAGGTGAGATCCCTGGTGAACACGGGCTAACCTGTATG	
PI	OSAMU KURAHASHI, TSUYOSHI NAKAMATSU, SHINICHI SUGIMOTO, PC C12N15/60, C12N15/54, C12N15/53, C12N15/31, C12N9/88, PC C12N9/12,			QY 905 AACGTGACTGGCTCACTGCGCTGCGGATACACTGGAGAAGTTGTGATACACCTTTATG	
PC	C12N9/04, C07R14/34, C12N9/26, C12N13/04			Db 1024 CCAGGACATCGAGGTGAGATCCCTGGTGAACACGGGCTAACCTGTATG	
CC	Key Location/Qualifiers			QY 905 AACGTGACTGGCTCACTGCGCTGCGGATACACTGGAGAAGTTGTGATACACCTTTATG	
FT	CDS (319) . (3735)			Db 1024 CCAGGACATCGAGGTGAGATCCCTGGGAGATCCGGCACCCTGCCCCAGC 1084	
FEATURES	Location/Qualifiers			Db 1024 CCAGGACATCGAGGTGAGATCCCTGGGAGATCCGGCACCCTGCCCCAGC 1084	
source	1. . 4013				

Db	3242	CGAAGCCGACCGAGGGAGTTCTTGAAGCACCGTGGCCCTGCTGGCAACACCTCCGCCCTGG	3301
Qy	3185	ATGATCGTGAATTCTCTAACG3CCCTGGCTGAAGGCCGGAGACTTGTATCCGGCTGCCAG	3244
Db	3302	ATGACCGCGAGTTCTACGGCTTGAAAGGGACGTGAGGGCTGACTGACCTGACCG	3361
Qy	3245	ATGTGCACCCCACTGCTGCTGGATGCGATCTCTGAGCAGACGATAAGGTA	3304
Db	3362	GTGTGTCACCCCGATGGTGGTCGGCTGGATGGGGTGTCCGAACCGATGACAAAGGCA	3421
Qy	3305	TGGCAATGTTGGCCAACGTCAACGGCAAGATCCGCCAATGCTGTTGACCGCT	3364
Db	3422	TGGCAACGGTGGTCAACGTCAACGGCAAGATCCGGCGATCAAGTGGGACCGTT	3481
Qy	3365	CGTTGAGTCGTCAACCGCAAACGGCAGAAAAGGGAGATTCCTCCAAACAAGGGCATGTTG	3424
Db	3482	CGTGGAGTCGGTACCGGCCACCGGGAGAAGGGCGATGCCACCAACAAGGGCATGTCG	3541
Qy	3425	CTGCAACATTGCTGGTGTACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTG	3484
Db	3542	CCGACCCATTGCCGGTGTGGTACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTG	3601
Qy	3485	GAGATGCACTGCAATTATCGAGGGCTATGAAAGATGGAAGAACATCACTGCTTCTGTTG	3544
Db	3602	GCGACGCCGTGGCCATCATGGGCCATGAAAGATGGGGCCACCATTGAGGTGAGGTCAAGGCTG	3661
Qy	3545	ACGGCAAATCGATGCGTTGGGTTCTGCTGCAACGAAGGTGGAAAGGTGGGACTTGA	3604
Db	3662	ACGGTGTCACTGACCGCGTGTGGTCCGGCCACCAAGGTGAGGGGGGACCTCA	3721
Qy	3605	TGTCGTCGTTGGTTCCCA	3620
Db	3722	TGTCGTCGTTCCCA	3737

Search completed: March 24, 2004, 00:13:39
 Job time : 13746 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

DBM nucleic - nucleic search, using SW model

Run on: March 23, 2004, 17:20:33 ; Search time 1295 Seconds
(without alignments)
11878.552 Million cell updates/sec

Title: US-10-045-072-1
Perfect score: 3621
Sequence: 1 tgggggggttagatccctg.....tgtatcgtcgtcgttcccaa 3621

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

ALIGNMENTS

RESULT 1
AAA47533
ID AAA47533 standard; DNA; 3621 BP.
XX
AC AAA47533;
XX DT 20-OCT-2000 (first entry)
XX DE Sequence encoding pyruvate carboxylase of C. glutamicum.
XX KW pyruvate carboxylase; expression; amino acid biosynthesis; lysine;
KW glutamic acid; oxaloacetate; fermentation; biosynthesis; ds.
XX

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

SUMMARIES						
Result	No.	Score	Query	Match	Length	DB ID
	1	3621	100.0	3621	3	AAA47533
	2	3621	100.0	3621	5	AAF32165
	3	3621	100.0	3621	6	AAD42046
	4	3621	100.0	3621	8	ACA62133
	5	3621	100.0	349980	5	AAH68526
	6	3576.4	98.8	3728	2	AAX24102
	7	3420	94.4	3420	5	AAH65730
	8	3398.8	93.9	3474	6	ABR52832
	9	2279.6	63.0	4013	5	AAF87437
	10	1927.4	53.2	3423	7	ACA29831
	11	1708	47.2	1719	4	AAF71419
	12	1395	38.5	1406	4	AAF71420
	13	1361.6	37.6	3381	7	ACA37896
	14	1294.4	35.7	3384	7	ACA40756
	15	1294.4	35.7	110000	4	AAI99682-33
	16	1294.4	35.7	110000	4	AAI99683-33
	17	1292.2	35.7	3381	7	ACA38630-
	18	1249.6	34.5	32155	9	ADB74252
C	19	1033	28.5	1083	4	AAF71418
C	20	1033	28.5	1083	4	AAF71417
	21	907	25.0	939	4	AAF71415
	22	907	25.0	939	4	AAF71416

producing amino acids, preferably lysine and glutamic acid in industrial

Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;						
Query	Match	Score	DB	Length	3621;	
Best Local	Similarity	100.0%	Pred.	No.	0;	
Matches 3621;	Conservative	0;	Mismatches	0;	Indels	0;
					Gaps	0
1	TGGGGGGGTAGATCCTGGGGTTATTCAATTCACTTGGCTTGAAAGTCGTGCCAGG	60				
1	TGGGGGGTTAGATCCTGGGGTTATTCACTTGGCTTGAAAGTCGTGCCAGG	60				
61	TCAGGGGAGTGTGAAACATTGAGGGAAAACAAAAACCGATGTTGATTGGGG	120				
61	TCAGGGGAGTGTGCCGAAACATTGAGGGAAAACAAAAACCGATGTTGATTGGGG	120				
121	AATCGGGGTTACCATTAACGGGAACTGACTCACACATCACCCTTGGCGGTCTCTTG	180				
121	AATCGGGGTTACGATACTAGGACGGACTCACACATCACCCTTGGGGTCTCTTG	180				
181	AAAGGAATAATTACTCTAGTGTGACTCACACATCCTAACGCTTCCCAGCATTCAAAAG	240				
181	AAAGGAATAATTACTCTAGTGTGACTCACACATCCTAACGCTTCCCAGCATTCAAAAG	240				
241	ATCTTGGTAGCCAAACGGGGAAATCGGGGTACCGTCTCGGTGAGGCACTCGAAACC	300				
241	ATCTTGGTAGCCAAACGGGGAAATCGGGGTACCGTCTCGGTGAGGCACTCGAAACC	300				
301	GGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCACCGCTCTTT	360				
301	GGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCACCGCTCTTT	360				
361	GCTTCTGAAGCTCGCATTTGGTACCGAAGGGCTCACCAAGGTACCTGGACATC	420				
361	GCTTCTGAAGCTCGCATTTGGTACCGAAGGGCTCACCAAGGTACCTGGACATC	420				
421	GATGAAATTATCGGTGAGCTTAAGGAGATGCCATTACCGGATAACGGC	480				
421	GATGAAATTATCGGTGAGCTTAAGGAGATGCCATTACCGGATAACGGC	480				
481	TTCCTGCTGAAATGCCAGCTTGGCCGAGGTGTGGGAAACGGCATTACCTTAT	540				
481	TTCCTGCTGAAATGCCAGCTTGGCCGAGGTGTGGGAAACGGCATTACCTTAT	540				
541	GGCCCAACCCAGGGTTCTGATCTACCGGTATAAGTCTCGGGGTAAACCGCCCG	600				
541	GGCCCAACCCAGGGTTCTGATCTACCGGTATAAGTCTCGGGGTAAACCGCCCG	600				
601	AAGAAGGCTCTGCCAGTTGGCGGAATCCACCCGGAGCAAACATCGATGAGATC	660				
601	AAGAAGGCTGGCTGGCAAGCTTGGGAATCCACCCGGAGCAAACATCGATGAGATC	660				
661	GTAAAGGGCTGAAGGCCAGACTTACCCATCTTGTGAAGGGCAGTGGCTGGCC	720				
661	GTAAAGGGCTGAAGGCCAGACTTACCCATCTTGTGAAGGGCAGTGGCTGGCC	720				
721	GGACGGGCTATGGCTTGGCTGAGCTTGGCTGAGCTTGGCTGGCTGTGATGAGCT	780				
721	GGACGGGCTATGGCTTGGCTGAGCTTGGCTGAGCTTGGCTGGCTGTGATGAGCT	780				
781	TCTCGTGAAGCTGCTCACTGCAGGGCTTTGGCTGAGCTTGGCTGGCTGTGAT	840				
781	TCTCGTGAAGCTGCTCACTGCAGGGCTTTGGCTGAGCTTGGCTGGCTGTGAT	840				
841	AACCTCAGCATATTGAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCT	900				
841	AACCTCAGCATATTGAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTACACCT	900				
901	TATGAACCGTGAAGCTGCTCACTGCAGGGCTTTGGCTGAAATTGGCCAGCA	960				

Db	901	TATGAACTGGACTGCTCACTGCAGCGTCCACCGGTGATGCCATTGGCATTCGAAATGGCCAGGCA	960
Qy	961	CAGCATTGGATCCAGAACCTGGCTGATGCCATTGGCATTCGAAATGGCCAGGCA	1020
Db	961	CAGCATTGGATCCAGAACCTGGCTGATGCCATTGGCATTCGAAATGGCCAGGCA	1020
Qy	1021	TCCATTGGTTACCGGGCGGGAAACCGTGGAAATTCTGGTCGATGAAAGGGCAACCAC	1080
Db	1021	TCCATTGGTTACCGGGCGGGAAACCGTGGAAATTCTGGTCGATGAAAGGGCAACCAC	1080
Qy	1081	GTCCTTCATCGAAATGAAACCCACCGTATCCAGGTTGAGCACCCGTAAGGAAGTCACC	1140
Db	1081	GTCCTTCATCGAAATGAAACCCACCGTATCCAGGTTGAGCACCCGTAAGGAAGTCACC	1140
Qy	1141	GAGGTGGACCTGGTGAAGGGCGAGATGGCCTGGCTGCTGGCAACCTTGAAAGGAATTG	1200
Db	1141	GAGGTGGACCTGGTGAAGGGCGAGATGGCCTGGCTGCTGGCAACCTTGAAAGGAATTG	1200
Qy	1201	GCTCTGACCCAAAGATAAGATCAAGAACCCACGGGTGAGGACTCTGCAGTGGCATCACCAG	1260
Db	1201	GCTCTGACCCAAAGATAAGATCAAGAACCCACGGGTGAGGACTCTGCAGTGGCATCACCAG	1260
Qy	1261	GAAGATCCAACAAACGGGTTCCGGCCAGATAACCGGAACATACCGGCTCACCA	1320
Db	1261	GAAGATCCAACAAACGGGTTCCGGCCAGATAACCGGAACATACCGGCTCACCA	1320
Qy	1321	GGCGGAGCTGGCCTTGTGCTTGTGCTGGCTGAGCTAGCTGGTGGGAAATACCGGCACAC	1380
Db	1321	GGCGGAGCTGGCCTTGTGCTTGTGCTGGCTGAGCTAGCTGGTGGGAAATACCGGCACAC	1380
Qy	1381	TTTGACTCCATGGTGAATAACCTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATTGGTTTC	1440
Db	1381	TTTGACTCCATGGTGAATAACCTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATTGGTTTC	1440
Qy	1441	CGTGCACAGGGCGTTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATTGGTTTC	1500
Db	1441	CGTGCACAGGGCGTTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATTGGTTTC	1500
Qy	1501	TTGGCTGGTTGCTGGGAAAGGGACTTCACTTCCAAGGGCATGCCAACCGGATTCACTT	1560
Db	1501	TTGGCTGGTTGCTGGGAAAGGGACTTCACTTCCAAGGGCATGCCAACCGGATTCACTT	1560
Qy	1561	GCGGATCACCCGCACCTCCTCAGGTGACGGTCAACCTGCTGATGAGCAGGGCATCCTG	1620
Db	1561	GCGGATCACCCGCACCTCCTCAGGTGACGGTCAACCTGCTGATGAGCAGGGCATCCTG	1620
Qy	1621	GATTACTGGCAGATGTCAACCGTGAACAAGGCCTCATGGTGTGGTCCAAGGATGTTGCA	1680
Db	1621	GATTACTGGCAGATGTCAACCGTGAACAAGGCCTCATGGTGTGGTCCAAGGATGTTGCA	1680
Qy	1681	GCTCCTATCGATAAGCTGCCAACATCAAGGATCTGCCACTTGGCTGAGCAGGACGGTCCG	1740
Db	1681	GCTCCTATCGATAAGCTGCCAACATCAAGGATCTGCCACTTGGCTGAGCAGGACGGTCCG	1740
Qy	1741	GGCCTGAAGCAGCTTGGCCCAGCCGGCTTGTGCTGAGCAGGACGGCACTG	1800
Db	1741	GGCCTGAAGCAGCTTGGCCCAGCCGGCTTGTGCTGAGCAGGACGGCACTG	1800
Qy	1801	GCAGTTTACTGATAACCCTTCGGCATGCCAACAGTCTTGTGCTGGACCCGGAGTCCGC	1860
Db	1801	GCAGTTTACTGATAACCCTTCGGCATGCCAACAGTCTTGTGCTGGACCCGGAGTCCGC	1860
Qy	1861	TCATTGCACTGAAGCCTGGCAAGGGCAAGGGCGACTACGATGTGGGATCTCTGAGCTTGTCC	1920
Db	1861	TCATTGCACTGAAGCCTGGCAAGGGCAAGGGCGACTACGATGTGGGATCTCTGAGCTTGTCC	1920
Qy	1921	GTGGAGGGCTTGGGGGGGGGAACTACGATGTGGGATCTCTGAGCTTGTCC	1980
Db	1921	GTGGAGGGCTTGGGGGGGGGAACTACGATGTGGGATCTCTGAGCTTGTCC	1980
Qy	1981	TGGGACAGGCTCGGAGGGCTGGGAGGGCGATGCCAATGTAACATTCAAGATGCTGCTT	2040
Db	1981	TGGGACAGGCTCGGAGGGCTGGGAGGGCGATGCCAATGTAACATTCAAGATGCTGCTT	2040

QY	2041	CGGGCCGCAACACCGTGGGATAACACCCGTACCCAGACTCCGTCGGCGGTTGTT	2100	QY	3121	TTCCTCGAAGCCAACCGAACAGAGTTCCCTGAGGCCGCTTCGGAAACACCTCTGCG	3180
Db	2041	CGGGCCGCAACACCGTGGGATAACACCCGTACCCAGACTCCGTCGGCGGTTGTT	2100	Db	3121	TTCCTCGAAGCCAACCGAACAGAGTTCCCTGAGGCCGCTTCGGAAACACCTCTGCG	3180
QY	2101	AAGGAAGCTGCCAGCTCGGCATCTTCGACGGCTTAACGAGCTC	2160	QY	3181	CTGGATGATCGTAATTCTTGAAAGGCCGGAGACTTGTATCCGGCT	3240
Db	2101	AAGGAAGCTGCCAGCTCGGCATCTTCGACGGCTTAACGAGCTC	2160	Db	3181	CTGGATGATCGTAATTCTTGAAAGGCCGGAGACTTGTATCCGGCT	3240
QY	2161	TCCCCAGATGCCAGCAATGACGCCAGTCTGGAGAACCAAACACCGCGGTAGGCCAGGTG	2220	QY	3241	CCAGATGTGCCACCCCCCATCTGCTTGCTGGATGCGATCTCTGAGCCAGACATAAG	3300
Db	2161	TCCCCAGATGCCAGCAATGACGCCAGTCTGGAGAACCAAACACCGCGGTAGGCCAGGTG	2220	Db	3241	CCAGATGTGCCACCCCCCATCTGCTTGCTGGATGCGATCTCTGAGCCAGACATAAG	3300
QY	2221	GCTATGGCTTATTCTGGTATCTCTGATCTCTGATCTCACCCCTGGATTAC	2280	QY	3301	GGTATGCGCAATTGTTGTGGCCAACGCCAATGCGTAGTCCAAACAGGCCAT	3360
Db	2221	GCTATGGCTTATTCTGGTATCTCTGATCTCACCCCTGGATTAC	2280	QY	3361	CGCTCCGGTGAATGCTGTCAACCGAACCGAGAAAGGCCAT	3420
QY	2281	TACCTAAAGGATGGCAAGGGAGATCGTCAAGTCTGGCCATTTAAGGGT	2340	Db	3361	CGCTCCGGTGAATGCTGTCAACCGAACCGAGAAAGGCCAT	3420
Db	2281	TACCTAAAGGATGGCAAGGGAGATCGTCAAGTCTGGCCATTAGGAT	2340	QY	3421	GTTGCTGCACCAATTGCGTGTGACTGTTGCTGAAGGTATGAGGTCAAG	3480
QY	2341	ATGGCTGGTCTGCTTCGCCCAGCTGGTAACCAAGGTGGTCACTTTGGCCATTAGGAT	2340	Db	3421	GTTGCTGGCACCATTGCGTGTGACTGTTGCTGAAGGTATGAGGTCAAG	3480
Db	2341	ATGGCTGGTCTGCTTCGCCCAGCTGGTAACCAAGGTGGTCACTTTGGCCATTAGGAT	2340	QY	3481	GCTGGAGATGCACTGGCAATCATCGAGGCTATGAGATGGAAACATCACTGCTCT	3540
QY	2401	TTCGATCTGCCAGTGACGTGCAACCCACGACTGGGGTGGCAGCTGGCAACCTAC	2400	Db	3481	GCTGGAGATGCACTGGCAATCATCGAGGCTATGAGATGGAAACATCACTGCTCT	3540
Db	2401	TTCGATCTGCCAGTGACGTGCAACCCACGACTGGGGTGGCAGCTGGCAACCTAC	2400	QY	3541	GTTGACGGCAAATAATGATCGATCGGTTGCTGCTGCAACGAAGGTGGGAC	3600
QY	2461	TTTGCTGCAAGCTGGTGGAGATGCTGGTGGAGCTGGTGGTGGCTGGC	2460	Db	3541	GTTGACGGCAAATAATGATCGATCGGTTGCTGCTGCAACGAAGGTGGGAC	3600
Db	2461	TTTGCTGCAAGCTGGTGGAGCTGGTGGTGGCTGGCTGGC	2460	QY	3601	TTGATCGTCGTGTTCTCAA	3621
QY	2521	ACCACTCCCAGCCAACCTCTGCACTGGCACACCCAGACACTGGGGTGGCGAT	2580	Db	3601	TTGATCGTCGTGTTCTCAA	3621
Db	2521	ACCACTCCCAGCCAACCTCTGCACTGGCACACCCAGACACTGGGGTGGCGAT	2580	RESULT 2			
QY	2581	ACGGTTTGAGGCTCGAGGGTGTGTTCTGACTCTGAGCCGTACTGGAAAGCAGGGCA	2640	AAF32165;			
Db	2581	ACGGTTTGAGGCTCGAGGGTGTGTTCTGACTCTGAGCCGTACTGGAAAGCAGGGCA	2640	ID	AAF32165 standard; DNA; 3621 BP.		
QY	2641	CTGTACCTGCCATTGAGTCTGGAACCCAGGCCAACCGGTCTACGCCACGAA	2700	XX			
Db	2641	CTGTACCTGCCATTGAGTCTGGAACCCAGGCCAACCGGTCTACGCCACGAA	2700	XX	12-APR-2001 (first entry)		
QY	2701	ATCCCAGGGGACAGTGTCCAACCTGTGCAAGGGCACCTGGCTGGGAT	2760	DE	Corynebacterium glutamicum pyruvate carboxylase coding sequence.		
Db	2701	ATCCCAGGGGACAGTGTCCAACCTGTGCAAGGGCACCTGGCTGGGAT	2760	XX	Pyruvate carboxylase; anaplerotic pathway; industrial fermentation; oxaloacetate; db.		
QY	2761	CGTTTCGAACTCATCGAAGACAACATCGCAGCCGTTAATGAGATGCTGGGACGCCAAC	2820	XX	Corynebacterium glutamicum.		
Db	2761	CGTTTCGAACTCATCGAAGACAACATCGCAGCCGTTAATGAGATGCTGGGACGCCAAC	2820	OS			
QY	2821	AAGGTCAACCCATCCTCGAAGGTGTTGGCAGCTCGACTCCACCTCGTGGGGT	2880	XX			
Db	2821	AAGGTCAACCCATCCTCGAAGGTGTTGGCAGCTCGACTCCACCTCGTGGGGT	2880	PD	09-JAN-2001.		
QY	2881	GTGGATCAGGAGACTTGTGCGATCCACAAAGTAGACGACATCCAGACTGTGTCATC	2940	XX	23-DEC-1998; 98US-00220081.		
Db	2881	GTGGATCAGGAGACTTGTGCGATCCACAAAGTAGACGACATCCAGACTGTGTCATC	2940	PR	23-DEC-1998; 98US-00220081.		
QY	2941	GCGGCACTGGAAAGCCGGCTCGAGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3060	PA	(MASS) MASSACHUSETTS INST TECHNOLOGY.		
Db	2941	GCGGCACTGGAAAGCCGGCTCGAGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3060	PI	Sinskey AJ, Lessard PA, Willis LB;		
QY	3001	CGGGCACTGGAAAGCCGGCTCGAGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3120	XX	WPI; 2001-122330/13.		
Db	3001	CGGGCACTGGAAAGCCGGCTCGAGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3120	DR	P-PSDB; AAB67129.		
QY	3061	CAGGGCACCTCGACGGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3120	XX	Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium glutamicum, for replenishing oxaloacetate consumed during lysine and glutamic acid production in industrial fermentations.		
Db	3061	CAGGGCACCTCGACGGCTGATTCCAAGGAACGTCGAACGCCCTGCG	3120	XX	Claim 2; Col 23-30; 29pp; English.		
PS				PS			

Page 4

The present invention provides the protein and coding sequences of the Corynebacterium glutamicum pyruvate carboxylase protein. This is an enzyme in the anaplerotic pathway. It can be used in the replenishment of oxaloacetate consumed during lysine and glutamic acid production in industrial fermentation.

Db	1981	TGGGACAGGCTCGACGGAGCTGGCCAGGGGATGCCGAAATGTAAACCATTCAGATGCTGCTT	2040
Qy	2041	CGGGCCGGAAACACCGTGGGATAACACCCGTACCCAGACTCCGTCTGCCGGGTTGGT	2100
Db	2041	CGGGCCGGAAACACCGTGGGATAACACCCGTACCCAGACTCCGTCTGCCGGGTTGGT	2100
Qy	2101	AAGGAAGCTGCCAGCTCGGGGTGACATCTCCGATCTTGACCGCCTAACGAGTC	2160
Db	2101	AAGGAAGCTGCCAGCTCGGGGTGACATCTCCGATCTTGACCGCCTAACGAGTC	2160
Qy	2161	TCCCAGATGGCTCCAGGAATCGACGCCAGTCCGGAGACCAACACCGGGTAGCCGAGGTG	2220
Db	2161	TCCCAGATGGCTCCAGGAATCGACGCCAGTCCGGAGACCAACACCGGGTAGCCGAGGTG	2220
Qy	2221	GCTATGGCTTATTCTGGTGAATCTGATCCAATGAAAAGCTTACACCCCTGGATTAAC	2280
Db	2221	GCTATGGCTTATTCTGGTGAATCTGATCCAATGAAAAGCTTACACCCCTGGATTAAC	2280
Qy	2281	TACCTAAAGATGGCAGAGGAGATCGCTCAAGTCTGGGCTCACATCTGGCATTAAAGGAT	2340
Db	2281	TACCTAAAGATGGCAGAGGAGATCGCTCAAGTCTGGGCTCACATCTGGCATTAAAGGAT	2340
Qy	2341	ATGGCTGGTCTGCTTGCCTTCAGCTGGGACTACCGGACTCTGGGTCAACGGTCAAAG	2400
Db	2341	ATGGCTGGTCTGCTTGCCTTCAGCTGGGACTACCGGACTCTGGGTCAACGGTCAAAG	2400
Qy	2401	TTCGATCTGCCAGTGCACGTGCAACCCACGACAATGGGTTGGCCAGCTGGCAACCTAC	2460
Db	2401	TTCGATCTGCCAGTGCACGTGCAACCCACGACAATGGGTTGGCCAGCTGGCAACCTAC	2460
Qy	2461	TTTGGCTGAGCTCAAGTGGCTGAGATGCTGGTGTGCTGGTGTGCTGGTGTGCTGGC	2520
Db	2461	TTTGGCTGAGCTCAAGTGGCTGAGATGCTGGTGTGCTGGTGTGCTGGTGTGCTGGC	2520
Qy	2521	ACCACCTCCCAGCCATCCCTGCCATCCATGCCACACCCCGTGCCTGCGAT	2580
Db	2521	ACCACCTCCCAGCCATCCCTGCCATCCATGCCACACCCCGTGCCTGCGAT	2580
Qy	2581	ACCGGTTGAGCCTCGAGGCTGCTTCTGACCTCGAGCGTACTGGAAAGCACTGGG	2640
Db	2581	ACCGGTTGAGCCTCGAGGCTGCTTCTGACCTCGAGCGTACTGGAAAGCACTGGG	2640
Qy	2641	CTGTACCTGCCATTGAGCTCTGGAAACCCAGGCCAACCGGTGCTAACGCCACGAA	2700
Db	2641	CTGTACCTGCCATTGAGCTCTGGAAACCCAGGCCAACCGGTGCTAACGCCACGAA	2700
Qy	2701	ATCCCCAGGACAGTTGAGCTCTGGAAACCTCTGGGCTTGGGGAT	2760
Db	2701	ATCCCCAGGACAGTTGAGCTCTGGAAACCTCTGGGCTTGGGGAT	2760
Qy	2761	CGRTTCAACTCATCGAAGACAACCTCGGAGCCACCGGACTCTGGGGCTTGGGG	2820
Db	2761	CGRTTCAACTCATCGAAGACAACCTCGGAGCCACCGGACTCTGGGGCTTGGGG	2820
Qy	2821	AAGGTCAACCCCATCCTCCAGGAGACTTGTGGCCACCTCGAACCTCGTCATC	2880
Db	2821	AAGGTCAACCCCATCCTCCAGGAGACTTGTGGCCACCTCGAACCTCGTCATC	2880
Qy	2881	GTGGATCCAGGAGACTTGTGGCCAGCTCCAGACATCCAGACTCTGTCACTC	2940
Db	2881	GTGGATCCAGGAGACTTGTGGCCAGCTCCAGACATCCAGACTCTGTCACTC	2940
Qy	2941	CGGTTCTGGCGGGAGCTTGTGGTAACCCCTCCAGGTGGCTGGCCAGGCCACT	3000
Db	2941	CGGTTCTGGCGGGAGCTTGTGGTAACCCCTCCAGGTGGCTGGCCAGGCCACT	3000
Qy	3001	CGGGCACTGGAAAGGCCCTCCGAAGGCAAGGCCACCTCTGACGGAAGTCC	3060
Db	3001	CGGGCACTGGAAAGGCCCTCCGAAGGCAAGGCCACCTCTGACGGAAGTCC	3060
Qy	3061	CAGGGCACCTCGACGCTGATGATCCAAGGAACGTCGAATAGCCTCAACCGCCTG	3120
Db	3061	CAGGGCACCTCGACGCTGATGATCCAAGGAACGTCGAATAGCCTCAACCGCCTG	3120

XX Novel pyruvate carboxylase polypeptide, useful for replenishing PT oxaloacetate consumed for biosynthesis during growth, or lysine and PT glutamic acid production in industrial fermentation.

XX Disclosure; Col 23-30; 28pp; English.

SQ The present invention relates to novel pyruvate carboxylase proteins and polynucleotides encoding such proteins. Sequences of the invention are important anaplerotic enzymes for replenishing oxaloacetate consumed for biosynthesis during growth, or lysine and glutamic acid production in industrial fermentation. The present sequence is C. glutamicum pyruvate carboxylase DNA.

XX	781	TCTCGTGAAGCTGAGGGCTTCGGGATGGGGTATATGTCAACGTGGTGTGATT	840
PT	841	AACCTCAGCATATTGAAGTGCAGATCTTGGGATCACACTGGAAAGTTGACACCTT	900
PT	841	AACCTCAGCATATTGAAGTGCAGATCTTGGGATCACACTGGAAAGTTGACACCTT	900
PS	Db		
XX	901	TATGAACTGACTGCTCACTGCAGCTTGAGTCAACAAAAGTGTGAAATTGGCCAGCA	960
CC	901	TATGAACTGACTGCTCACTGCAGCTTGAGTCAACAAAAGTGTGAAATTGGCCAGCA	960
CC	901	TATGAACTGACTGCTCACTGCAGCTTGAGTCAACAAAAGTGTGAAATTGGCCAGCA	1020
CC	961	CAGGATTGGATCCAGAACTTGGTGAATGCATTTGCGGATTCAGTAAGTCTGCCGC	1020
CC	961	CAGGATTGGATCCAGAACTTGGTGAATGCATTTGCGGATTCAGTAAGTCTGCCGC	1020
XX	Db		
SQ Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;	1021	TCCATTGGTTACCAAGGGCGGGAACCGTGGAAATCTTGGTCAAAAGGGCAAACAC	1080
Query Match 100.0%; Score 3621; DB 6; Length 3621;	1021	TCCATTGGTTACCAAGGGCAAACAC	1080
Best Local Similarity 100.0%; Pred. No. 0;	Db		
Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy		
Qy 1 TGCGGGGGTTAGATCCTGGGGTTTATTCACTTCACTTGGCTTGAAGTCTGCGAGG	60	1081 GTCTCATCGAAATGAACCCACAGTATCCAGTTGAGCACACCGTGAAGTCACC	1140
Db 1 TGCGGGGGTTAGATCCTGGGGTTTATTCACTTCACTTGGCTTGAAGTCTGCGAGG	60	1081 GTCTCATCGAAATGAACCCACAGTATCCAGGTGAGCACACCGTGAAGTCACC	1140
Qy 61 TCAGGGGAAACATTGAGAGAAAACAAAAACCGATTTGATTGGGG	120	1141 GAGGTGGACCTTGGTGAAGCCAGATGGCCAGATGGCTGGTGGCAACCTTGAAGGAATTG	1200
Db 61 TCAGGGGAAACATTGAGAGAAAACATTGAGAGAAAACATTGAGAGAAAACATTGAGAG	120	1141 GAGGTGGACCTTGGTGAAGCCAGATGGCTGGTGGCAACCTTGAAGGAATTG	1200
Qy 121 ATTCGGGGTTACGATACTAGGAGGCACTGACTGCTATCACCTTGGGTTCTCTGTTG	180	1201 GGCTGACCCAAAGATAAGATCAAGACCCACGGCTACCGCTCACACAG	1260
Db 121 ATTCGGGGTTACGATACTAGGAGGCACTGACTGCTATCACCTTGGGTTCTCTGTTG	180	1201 GGCTGACCCAAAGATAAGATCAAGACCCACGGCTACCGCTCACACAG	1260
Qy 181 AAGGAAATTAACTCTAGTGTCACTCACACATCTAACGCTTCCAGGATTCAAAAG	240	1261 GAAGATCCAAACAAACGGCTTCGGCCCCAGATAACGGGAACTATCACCGGTACCGCTACCA	1320
Db 181 AAGGAAATTAACTCTAGTGTCACTCACACATCTAACGCTTCCAGCATTCAAAAG	240	1261 GAAGATCCAAACAAACGGCTTCGGCCCCAGATAACGGGAACTATCACCGGTACCGCTACCA	1320
Qy 241 ATCTTGGTAGCAGGGGGAAATCGGGTCCGTGCTTTCGGCAGGACTCGAAACC	300	1321 GCGGGAGCTGGGTTCTGCTCTGACGGTCAAGCTCAGCTGGTGGCAAAATCACGGCAC	1380
Db 241 ATCTTGGTAGCAAACCGGGAAATCGGGTCCGTGCTTTCGGCAGGACTCGAAACC	300	1321 GCGGGAGCTGGGTTCTGCTCTGACGGTCAAGCTCAGCTGGTGGCAAAATCACGGCAC	1380
Qy 301 GGTGAGCCACGGTAGCTATTACCCCCGTGAAGATGGGGATCATTTCCACCGCTCTTT	360	1381 TTTCGACTCCATGCTGGTAAATGACTCTGGCTTCCGACTTTGCTGTGTTGCTGTGCT	1440
Db 301 GGTGAGCCACGGTAGCTATTACCCCCGTGAAGATGGGGATCATTTCCACCGCTCTTT	360	1381 TTTCGACTCCATGCTGGTAAATGACTCTGGCTTCCGACTTTGCTGTGTTGCTGTGCT	1440
Qy 361 GCCTTCTGAAGCTGTCGGCATTTGGTACCGAAGGCTCACCAACTAAGGGTACCTGGACATC	420	1441 CGTGCACAGCGCGGTTGCTGGTAAATGACTCTGGCTTCCACCGCTCTGGTGGCT	1500
Db 361 GCCTTCTGAAGCTGTCGGCATTTGGTACCGAAGGCTCACCAACTAAGGGTACCTGGACATC	420	1441 CGTGCACAGCGCGGTTGCTGGTAAATGACTCTGGCTTCCACCGCTCTGGTGGCT	1500
Qy 421 GATGAAATTATCGGTGAGCTAAAGTTAAAGCTGCCATTACCGGGATAACGGC	480	1501 TTGGCTGGCTTCCGACTTCAAGGGCTTCCGACTTCAAGGGCTTCCGACTTCAAGGGCTT	1560
Db 421 GATGAAATTATCGGTGAGCTAAAGTTAAAGCTGCCATTACCGGGATAACGGC	480	1501 TTGGCTGGCTTCCGACTTCAAGGGCTTCCGACTTCAAGGGCTTCCGACTTCAAGGGCTT	1560
Qy 481 TTCCCTGTGAAATGCCCAGAGGTTCTTGTGATCTACCGGTACGGTACCTTTATT	540	1561 GCGGATCACCGGCACCTCCCTCAGGCTCCACCTGCTGATGATGATGAGCAGG	1620
Db 481 TTCCCTGTGAAATGCCCAGAGGTTCTTGTGATCTACCGGTACGGTACCTTTATT	540	1561 GCGGATCACCGGCACCTCCCTCAGGCTCCACCTGCTGATGATGATGAGCAGG	1620
Qy 541 GGCCCCAACCCAGAGGTTCTTGTGATCTACCGGTACGGTACCTTTATT	600	1621 GATTACTTGGAGATGTCACCTGGCTAACATCAAGGATCTGCCACTGCCACG	1680
Db 541 GGCCCCAACCCAGAGGTTCTTGTGATCTACCGGTACGGTACCTTTATT	600	1621 GATTACTTGGAGATGTCACCTGGCTAACATCAAGGATCTGCCACTGCCACG	1680
Qy 601 AAGAAGGGCTGGCTGGCAAGCTGGCTGGGAAATCCACCCCGAGGAAACATCGATGAGATC	660	1681 GCTCTTATCGATAAGCTGGCTAACATCAAGGATCTGCCACTGCCACG	1740
Db 601 AAGAAGGGCTGGCTGGCTGGCAAGCTGGCTGGGAAATCCACCCCGAGGAAACATCGATGAGATC	660	1681 GCTCTTATCGATAAGCTGGCTAACATCAAGGATCTGCCACTGCCACG	1740
Qy 661 GTTAAAAGGGCTGAAAGGCCAGACCTTACCCCATTTGTGAAGGGAGTTGGTGGGC	720	1741 CGCTCTGAAGCAGCTGGCTTCCGGCCAGCTGGCTGATCTCCGTGAGCAGGACGACTG	1800
Db 661 GTTAAAAGGGCTGAAAGGCCAGACCTTACCCCATTTGTGAAGGGAGTTGGTGGGC	720	1741 CGCTCTGAAGCAGCTGGCTTCCGGCCAGCTGGCTGATCTCCGTGAGCAGGACGACTG	1800
Qy 721 GGACGGGGTATGGTTCTACCTGATGAGCTTGGTGGCTGCAAGCTTGTGCT	780	1801 GGAGTTACTGATAACCTTCGGCCAGCTGGCTGATCTCCGTGAGCAGGACGACTG	1860
Db 721 GGACGGGGTATGGTTCTACCTGATGAGCTTGGTGGCTGCAAGCTTGTGCT	780	1801 GGAGTTACTGATAACCTTCGGCCAGCTGGCTGATCTCCGTGAGCAGGACGACTG	1920
Qy 781 TCTCGTGAAGCTGAAAGCCCTGGGGATGGGGAGGGCGTGGCTGAAACGTGGTGTGATT	840	1861 TCATTGCACTGAAAGCCCTGGGGATGGGGAGGGCGTGGCTGAAACGTGGTGTGATT	

1861	TCATTGGCACTGAAGCCTGGGGAGCCCTACGATGGCGATGCCAAGGCAAGGCAAGGCAACTCTGACTCCTGAGCTTTGTGCC	1920	
1921	GTGGAGGCCTGGGGGGCGACCTACGATGGCGATGCCAAGGCAACTCTGAGCTCGCTCG 1980		
b	1921	GTGGAGGCCTGGGGGGCGACCTACGATGGCGATGCCAAGGCAACTCTGAGCTCGCTCG 1980	
y	1981	TGGGACAGGCTGACGAGGCTGCGGATGCCAATGTAAACATTAGATGCTGCTT 2040	
b	1981	TGGGACAGGCTGACGAGGCTGCGGATGCCAATGTAAACATTAGATGCTGCTT 2040	
y	2041	CGGGGCCAACACCCGTACCCAGACTCCGATCTGGCTGGCGGTTTGTT 2100	
b	2041	CGGGGCCAACACCCGTACCCAGACTCCGATCTGGCTGGCGGTTTGTT 2100	
y	2101	AAGGAAGGCTCCAGCTCCGGGTGGACATCTCGCATACTTCGACGGCTTAAGCACGTC 2160	
b	2101	AAGGAAGGCTCCAGCTCCGGGTGGACATCTCGCATACTTCGACGGCTTAAGCACGTC 2160	
y	2161	TCCCAGATGGCTCCAGCAATCGACGAGCAACACCGGGTAGCCGAGGTG 2220	
b	2161	TCCCAGATGGCTCCAGCAATCGACGAGCAACACCGGGTAGCCGAGGTG 2220	
y	2221	GCTATGGCTTATCTGGTATCTCTGATCCAATGAAAAGCTCTACACCTGGATTAC 2280	
b	2221	GCTATGGCTTATCTGGTATCTCTGATCCAATGAAAAGCTCTACACCTGGATTAC 2280	
y	2281	TACCTAAAGATGGCAGAGGATCGTCAAGTCGGGCTCACATTTGGCATTAAAGGAT 2340	
b	2281	TACCTAAAGATGGCAGAGGATCGTCAAGTCGGGCTCACATTTGGCATTAAAGGAT 2340	
y	2341	ATGGCTGGTCTGGCTTGGGCTAACCAAGGTTAACCTGGCTAACATTAAAGGAT 2340	
b	2341	ATGGCTGGTCTGGCTTGGGCTAACCAAGGTTAACCTGGCTAACATTAAAGGAT 2340	
y	2401	TTCGATCTGCCAGTGGCACCGTGCACACCCACGACACTGGGGTGGCTAACCTAC 2460	
b	2401	TTCGATCTGCCAGTGGCACCGTGCACACCCACGACACTGGGGTGGCTAACCTAC 2460	
y	2461	TTTGCTGGAGCTCAAGCTGGCACACCCACGACACTGGGGTGGCTAACCTAC 2460	
b	2461	TTTGCTGGAGCTCAAGCTGGCACACCCACGACACTGGGGTGGCTAACCTAC 2460	
y	2521	ACCACTCCAGCCATCCCTGTCGAGATGCTGTCATTGCCACCCGTGGCAT 2520	
b	2521	ACCACTCCAGCCATCCCTGTCGAGATGCTGTCATTGCCACCCGTGGCAT 2520	
y	2581	ACGGTTTGAGCCTCGAGGCTGAGCTTGAGCTGGCAAGGCAAGGCAAGGCA 2640	
b	2581	ACGGTTTGAGCCTGAGCTGAGCTTGAGCTGGCAAGGCAAGGCAAGGCA 2640	
y	2641	CTGTACCTGCCATTGAGCTCTGGCACAGCCGCAACGCCACCGCA 2700	
b	2641	CTGTACCTGCCATTGAGCTCTGGCACAGCCGCAACGCCACCGCA 2700	
y	2701	ATCCCAAGGGACAGCTGTCCTGGCAACCTGGCTTAAATGAGATGCTGGCAT 2760	
b	2701	ATCCCAAGGGACAGCTGTCCTGGCAACCTGGCTTAAATGAGATGCTGGCAT 2760	
y	2761	CGTTTCAAGCAACTCATCGAAGACAACTACGCAAGCCGTTATGAGATGCTGGCAACCCGCA 2820	
b	2761	CGTTTCAAGCAACTCATCGAAGACAACTACGCAAGCCGTTATGAGATGCTGGCAACCCGCA 2820	
y	2821	AAGTCACCCCATCCTCCAGGTTGGCGACCTCGCACTCCACCTCCAGACATCCAGACTCTGTCACTC 2940	
b	2821	AAGTCACCCCATCCTCCAGGTTGGCGACCTCGCACTCCACCTCCAGACATCCAGACTCTGTCACTC 2940	
y	2881	GTGGATCCAGCAGACTTGGCTGCCATCCACAAAGTACGACATCCAGACTCTGTCACTC 2940	
b	2881	GTGGATCCAGCAGACTTGGCTGCCATCCACAAAGTACGACATCCAGACTCTGTCACTC 2940	
y	2941	GGTTTCTGGGGAGCTTGGCTGCCAGGCAACTGGGCAACTGGGCA 3000	
b	2941	GGTTTCTGGGGAGCTTGGCTGCCAGGCAACTGGGCAACTGGGCA 3000	

PR	23-DEC-1998;	98US-00220081.	Qy	601	AAGAAGGGCTGGTCTGCCAGTTGGGAATCCACCCGAGCAAAACATCGATGAGATC	660	
PR	03-OCT-2000;	2000US-00677575.	Db	601	AAGAAGGGCTGGTCTGCCAGTTGGGAATCCACCCGAGCAAAACATCGATGAGATC	660	
XX	(ARCH) ARCHER-DANIELS MIDLAND CO.						
PA	XX	Sinskey AJ, Lessard PA, Willis LB;					
PT	XX	WPI; 2003-479542/58.					
PT	DR	P-PSDB; ABU10426.					
XX	XX	New pyruvate carboxylase from <i>Corynebacterium glutamicum</i> , useful as an anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis during growth, or for lysine or glutamic acid production in industrial fermentations.					
PT	XX	PS	Claim 2 ; Page 12-16; 29pp; English.				
CC	CC	The invention describes a new isolated pyruvate carboxylase polypeptide having an amino acid sequence at least 95% identical to a sequence comprising 1140 amino acids from <i>Corynebacterium glutamicum</i> , or the complete amino acid sequence encoded by the cosmid clone deposited with the American Type Culture Collection. The polypeptide is useful as an anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis during growth. The polypeptide is also useful for lysine or glutamic acid production in industrial fermentations. This sequence encodes <i>Corynebacterium glutamicum</i> pyruvate carboxylase.					
CC	CC	Sequence 3621 BP; 782 A; 1037 C; 1002 G; 800 T; 0 U; 0 Other;					
Query	Match	100.0%; Score 3621; DB 8; Length 3621;					
Best Local Similarity	100.0%; Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;					
Matches 3621; Conservative 0;							
Qy	1	TGGGGGGGTAGATCCTGGGGTTATTCACTTCAACTTGGCTTGAAAGTCGTGCAGG	60	Qy	901	TATGAACTGTGACTGCTCACTGGCGTCAACCAAAAGTGTGAAATTGAGAAGTGCAGCA	960
Db	1	TGGGGGGGTAGATCCTGGGGTTATTCACTTCAACTTGGCTTGAAAGTCGTGCAGG	60	Db	901	TATGAACTGTGACTGCTCACTGGCGTCAACCAAAAGTGTGAAATTGAGAAGTGCAGCA	960
Qy	61	TCAGGGGAGTGGTTGCCCGAAAAACATTGAGGGAAAACATTGAGATTTGATTGGGG	120	Qy	961	CAGCATTGGATCCCGAACCTGGTGAACGGTGGCATTCAGTAAAGTGTGCGGATTCAGTA	1020
Db	61	TCAGGGGAGTGGTTGCCCGAAAAACATTGAGGGAAAACATTGAGATTTGATTGGGG	120	Db	961	CAGCATTGGATCCCGAACCTGGTGAACGGTGGCATTCAGTAAAGTGTGCGGATTCAGTA	1020
Qy	121	AATCGGGGGTACGATACTAGGACCGTAGTGTACTGCTATCACCCCTGGGGTCTCTTGTG	180	Qy	1021	TCCATTGGTTACCGGGGGAAACGTGGAATTCTTGGTCTGATGAAACGGCAACCAC	1080
Db	121	AATCGGGGGTACGATACTAGGACCGTAGTGTACTGCTATCACCCCTGGGGTCTCTTGTG	180	Db	1021	TCCATTGGTTACCGGGGGAAACGTGGAATTCTTGGTCTGATGAAACGGCAACCAC	1080
Qy	181	AAGGAAATAATTACTCTAGTGTGACTCACACATCTAACGCTTCCAGCATTCAGA	240	Qy	1081	GTCTTCATCGAAATGAACCCACGTGCTGGAATTCTGGTCTGAGTAAAGTGTGACCTACC	1140
Db	181	AAGGAAATAATTACTCTAGTGTGACTCACACATCTAACGCTTCCAGCATTCAGA	240	Db	1081	GTCTTCATCGAAATGAACCCACGTGCTGGAATTCTGGTCTGAGTAAAGTGTGACCTACC	1140
Qy	241	ATCTTGGTAGCAAACCGGGGGAAATCGGGTCCGTGCTTCCGGCAGCACTGAAACC	300	Qy	1201	GGTCTGACCCAAGATAAGATCAAGACCCACGGGTGAGACTGCGCATCACCCACG	1260
Db	241	ATCTTGGTAGCAAACCGGGGGAAATCGGGTCCGTGCTTCCGGCAGCACTGAAACC	300	Db	1201	GGTCTGACCCAAGATAAGATCAAGACCCACGGGTGAGACTGCGCATCACCCACG	1260
Qy	301	GGTGCAGCACGGTAGCTATTACCCCCGGTGAAGATCGGGATCATTCACCGCTCTTT	360	Qy	1261	GAAGATCCAAACAAACGGCTTCCGCCAGATAACCGGAACATACCCGTCACCA	1320
Db	301	GGTGCAGCACGGTAGCTATTACCCCCGGTGAAGATCGGGATCATTCACCGCTCTTT	360	Db	1261	GAAGATCCAAACAAACGGCTTCCGCCAGATAACCGGAACATACCCGTCACCA	1320
Qy	361	GCTTCTGAGTGGCTCGGCAATTGGTACCGGAAGGCTACCAAGTCAAGGGTACCTGGACATC	420	Qy	1321	GGCGGAGGCTGGGGTGTGCTGACGGTCAAGCTGGTGGGAAATCACCGCACAC	1380
Db	361	GCTTCTGAGTGGCTCGGCAATTGGTACCGGAAGGCTACCAAGTCAAGGGTACCTGGACATC	420	Db	1321	GGGGAGGCTGGGGTGTGCTGACGGTCAAGCTGGTGGGAAATCACCGCACAC	1380
Qy	421	GATGAAATAATTACGGTAGCTTACGGGAAATGGAGATGGCTACCCGGATACGGC	480	Qy	1381	TTTGACTCCATGCTGGTCAAGCTGGTCTGGTCTGGTCAAGCTGGTGTGCT	1440
Db	421	GATGAAATAATTACGGTAGCTTACGGGAAATGGAGATGGCTACCCGGATACGGC	480	Db	1381	TTTGACTCCATGCTGGTCAAGCTGGTCTGGTCTGGTCAAGCTGGTGTGCT	1440
Qy	481	TTCCCTGTCGAAATTGCCAGCTTGTGATCTGCCACCTTACCGGATACGGC	540	Qy	1441	CGTGCACAGCGCGCTGCTGGCTGAGTCAAGGCAATTGGTTTC	1500
Db	481	TTCCCTGTCGAAATTGCCAGCTTGTGATCTGCCACCTTACCGGATACGGC	540	Db	1441	CGTGCACAGCGCGCTGCTGGCTGAGTCAAGGCAATTGGTTTC	1500
Qy	541	GGCCCAACCCAGGGTTCTTGATCTACCCGGTAAAGTGTGCGGTAACCGCCGG	600	Qy	1501	TTGCGTGCCTCAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT	1620
Db	541	GGCCCAACCCAGGGTTCTTGATCTACCCGGTAAAGTGTGCGGTAACCGCCGG	600	Db	1501	TTGCGTGCCTCAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT	1620
Qy	1681	GCTCCCTATCGATAAGCTGCCAAACATCAAGGATCTGCCACTGCCAAAGGATCTGCC	1740	Qy	1621	GATTACTGGCAGATGCTCACCGTCAACGGTCAAGGATGTTGCA	1680
Db	1621	GATTACTGGCAGATGCTCACCGTCAACGGTCAAGGATGTTGCA	1680	Db	1621	GATTACTGGCAGATGCTCACCGTCAACGGTCAAGGATGTTGCA	1680

XX	EP1108790-A2.	Db	105433	GATGAAATTATCGGTGCAGCTAAAAGTTAAAGCAGATGCCATTACCCGGGATA CGGC 105492
XX	PD 20-JUN-2001.	QY	481	TTCCTGTCTGAAAATGCCAAGCTTGCCCGGAGTGTGGGA AACGGCAATTACTTTTATT 540
XX	PP 18-DEC-2000; 20000EP-00127688.	Db	105493	TTCCTGTCTGAAAATGCCAAGCTTGCCCGGAGTGTGGGA AACGGCAATTACTTTTATT 105552
XX	PR 16-DEC-1999; 99JP-00377484.	QY	541	GGCCAACCCCAAGAGTTCTTGATCTCACCGGTATAAGTCTCGGGCGTAACCGCGCG 600
XX	PR 07-APR-2000; 2000JP-00159162.	Db	105553	GGCCAACCCCAAGAGTTCTTGATCTCACCGGTATAAGTCTCGGGCGTAACCGCGCG 105612
XX	PR 03-AUG-2000; 2000JP-00280988.	QY	601	AAGAAGGTGGTCTGCCAGTTGGGAATCCACCCGAGAAAAACATCGATGAGATC 660
XX	PA (KYOW) KYOWA HAKKO KOGYO KK.	Db	105613	AAGAAGGTGGTCTGCCAGTTGGGAATCCACCCGAGAAAAACATCGATGAGATC 105672
XX	PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;	QY	661	GTAAAGGGCCAGACTAACCCATCTTGTGAAGGCAGTTGGCGTGGTGGC 720
XX	PI Tateishi N, Senoh A, Ikeda M, Ozaki A;	Db	105673	GTAAAGGGCCAGACTAACCCATCTTGTGAAGGCAGTTGGCGTGGTGGC 105732
XX	DR WPI; 2001-376931/40.	QY	721	GGACCGGGTATGGCTTACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 780
XX	PT Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.	Db	105733	GGACCGGGTATGGCTTACCTGATGAGCTTCGCAAATTAGCAACAGAAGCA 105792
XX	PS Disclosure; SEQ ID NO 7061; 24pp + Sequence Listing; English.	Db	105793	TCTCGTGAAGCTGAAGGGCCTTTCGGGATGGCCGGTATAATGTCGAACGTGCTGTGATT 840
XX	CC The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office	QY	841	AACCCTCAGCATATTGAACTGGCAGATCCTTGGCGATCACACTGGAGAACGTTGACACCTT 900
XX	CC	Db	105853	AACCCCTCAGCATATTGAACTGGCAGATCCTTGGCGATCACACTGGAGAACGTTGACACCTT 105912
PS	CC	QY	901	TATGAAACGTGACTGCTCACTGGCAGCTGCTCGTCAACCAAAAGTTGTGCGAACCCAGCA 960
XX	CC	Db	105913	TATGAAACGTGACTGCTCACTGGCAGATCCTGGCGTCAACCAAAAGTTGTGCGAACCCAGCA 105972
XX	CC	QY	961	CAGGATTTGGATCCAGAAACTGGTGTATCGGTGATTCGCAACTTGTGGGATGCAAGTAAGTTCTGCCGC 1020
CC	CC	Db	105973	CAGGATTTGGATCCAGAAACTGGTGTATCGGTGATTCGCAACTTGTGGGATGCAAGTAAGTTCTGCCGC 106032
SQ	Sequence 349980 BP; 79274 A; 90638 C; 98727 G; 81341 T; 0 U; 0 Other;	QY	1021	TCCATTGGTTACCGGGGGGGAAACCGTGGATACTTGGTGGATGAAAAGGGCAACAC 1080
XX	Query Match Score 100.0%; Score 3621; DB 5; Length 349980; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 3621; Conservative 0;	Db	106033	TCCATTGGTTACCGGGGGGGAAACCGTGGATACTTGGTGGATGAAAAGGGCAACAC 106092
QY	1 TGCCCCCTTAGATCTGCCGAAAAACATTGAGGGAAAAACATTGAGGGAAAAACATTGAGGGAAAAACATTGAGGGAAAAACATTGAGGGAAAAACATTGAGGG 60	QY	1081	GTCTTCATCGAAATGAACCCACGTATCCAGGTGACTGAAGAACTTCACC 1140
Db	105013 TGGGGGGTTAGATCTGCCGAAAAACATTGAGGGAAAAACATTGAGGGTTATTCTGGGGGTTATTCTACCTTGCTTAAGTCTGGCAG 105072	Db	106093	GTCTTCATCGAAATGAACCCACGTATCCAGGTGACTGAAGAACTTCACC 106152
QY	61 TCAGGGGGTTACGATACTAGGAGCCAGTGACTGCTATCACCTCAACATCTCAACGCTTCCAGGATTCAAAAG 120	QY	1141	GAGGTGGACCTGGTGAAGGGCAGATGCGCTGGTGCACCCGTGACTGAAGAACTTG 1200
Db	105073 TCAGGGGAGTGTGGTGCCTGGGGTTATTCTACCTTGCTTAAGTCTGGCAG 105132	Db	106153	GAGGTGGACCTGGTGAAGGGCAGATGCGCTGGTGCACCCGTGACTGAAGAACTTG 106212
QY	121 AATCGGGGGTTACGATACTAGTGTGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 180	QY	1201	GGTCTGACCTGGTGAAGGGCAGATGCGCTGGTGCACCCGTGACTGAAGAACTTG 1260
Db	105133 AATCGGGGGTTACGATACTAGTGTGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 105192	Db	106213	GGTCTGACCCAGATAAGTCAAGACCCACGGTGCAGCTGCAGTCCACCCAG 106272
QY	181 AAAGGAATAATTACTCTAGTGTGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 240	QY	1261	GAAGATCCAAACCAACGGGTTCCGGCCAGATACCGGAACATACTCCGGCTCACCA 1320
Db	105193 AAAGGAATAATTACTCTAGTGTGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 105252	Db	106273	GAAGATCCAAACCAACGGGTTCCGGCCAGATACCGGAACATACTCCGGCTCACCA 106332
QY	241 ATCTGGTAGCAAACCGGGCTCCGTTTCGAGGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 105312	QY	1321	GGGGAGCTGGCGGTTCTGACGGTGGCTAGCTGGTGGGGAAATCACCGCACAC 1380
Db	105253 ATCTGGTAGCAAACCGGGCTCCGTTTCGAGGACTCACACATCTCAACGCTTCCAGGATTCAAAAG 105372	Db	106333	GGGGAGCTGGCGGTTCTGACGGTGGCTAGCTGGTGGGGAAATCACCGCACAC 106392
QY	301 GGTGCAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTCCACCGCTCTTT 360	QY	1381	TTTGACTCCATGGTGTGAAATGACCTGGCTGGTGGGGAAATCACCGCACAC 1440
Db	105313 GGTGCAGCCACGGTAGCTATTACCCCGTGAAGATCGGGGATCATTCCACCGCTCTTT 105372	Db	106393	TTTGACTCCATGGTGTGAAATGACCTGGCTGGTGGGGAAATCACCGCACAC 106452
QY	361 GCTTCTGAAAGCTGTCGCAATTGGTACCGAAGGGTCAACAGTCGGTACCTGGACATC 420	QY	1441	CGTGCACAGGGCGGTTCTGGCTGAACCAAACATGGTTTC 1500
Db	105373 GCTTCTGAAAGCTGTCGCAATTGGTACCGAAGGGTCAACAGTCGGTACCTGGACATC 105432	Db	106453	CGTGCACAGGGCGGTTCTGGCTGAACCAAACATGGTTTC 106512
QY	421 GATGAAATTATCGGTGCAGCTAAAAGTTAAAGCAGATGCCATTACCCGGATA CGGC 480	QY	1501	TTGCGTGTGGTGTGCAAGGGATTCATTCCACCGGATTCATT 1560
Db	106513 TTGCGTGTGGTGTGCAAGGGATTCATTCCACCGGATTCATT 106572	Db		

Db	1390	TTGAAACTGCTGTGGCTCGCACAGGCCGTTGGCTGAGTTCACCGTGTCTGGTTG 1449
Qy	1484	CAACCAACATTGGTTCTTGCCTGGCTGAGGGACTTCACCTCCAAGGGCA 1543
Db	1450	CAACCAACATTGGTTCTTGCCTGGCTGAGGGACTTCACCTCCAAGGGCA 1509
Qy	1544	TGCCAACCGATTCAATTGCCATCACCCGACCTCCTCAGGCTCCACCTGGCTGATG 1603
Db	1510	TGCCAACCGATTCAATTGCCATCACCCGACCTCCTCAGGCTCCACCTGGCTGATG 1569
Qy	1604	AGCAGGGACGCATCCTGGATTAACTTGCCAGATGTACCCTGAACCAAGGCTCATGGTGTGC 1663
Db	1570	AGCAGGGAGGCATCCTGGATTAACTTGGCAGATGTACCCTGAACCAAGGCTCATGGTGTGC 1629
Qy	1664	GTCCAAGGGATAAGCTGAGCTCTTAACATCAAGGATCTGCACACTG 1723
Db	1630	GTCCAAGGGATAAGCTGCTCTTAACATCAAGGATCTGCACACTG 1689
Qy	1724	CACGGGGTTCCCCGTGAAGGCAGCTTGGCCAGGGCTTGGCTGATCTCC 1783
Db	1690	CACGGGGTTCCCCGTGAAGGCAGCTTGGCCAGGGCTTGGCTGATCTCC 1749
Qy	1784	GTGAGCAGGACGGCACTGGCAGTTACTGATAACCACCTTCGGGATGACACCCAGTCTTGC 1843
Db	1750	GTGAGCAGGACGGCACTGGCAGTTACTGATAACCACCTTCGGGATGACACCCAGTCTTGC 1809
Qy	1844	TTGCCACCCGAGTCCCGCTCATCGCACCTGAAAGCCTGGGGCAGAGGCCATGGCAAAGCTGA 1903
Db	1810	TTGCCACCCGAGTCCCGCTCATCGCACCTGAAAGCCTGGGGCAGAGGCCATGGCAAAGCTGA 1869
Qy	1904	CTCCTGAGCTTTGTCCGTGGAGGGCCTGGGGGGCACCTACGATGTGGGATGGCGTT 1963
Db	1870	CTCCTGAGCTTTGTCCGTGGAGGGCCTGGGGGGCACCTACGATGTGGGATGGCGTT 1929
Qy	1964	TCCTCTTTGAGGATCCCGTGGGACAGGGCTCGACGAGGCTGGGGGATGCCGAATGTAA 2023
Db	1930	TCCTCTTTGAGGATCCCGTGGGACAGGGCTCGACGAGGCTGGGGGATGCCGAATGTAA 1989
Qy	2024	ACATTCAAGATGCTGCTTCCGGGCAACACCCGTTGGGATAACACCCGTAACCCAGACTCCG 2083
Db	1990	ACATTCAAGATGCTGCTTCCGGGCAACACCCGTTGGGATAACACCCGTAACCCAGACTCCG 2049
Qy	2084	TCTGCCCGGGCTTTGTTAAGGAAGGCTGCCAGGCTGGGACATCTTCGGCATCTTCGG 2143
Db	2050	TCTGCCCGGGCTTTGTTAAGGAAGGCTGCCAGGCTGGGCTATGGCTTATCTGGGATCTTCGG 2109
Qy	2144	ACGCCCTTAACCGACGGTCTCCCAAGATCGCGCAATCGCACGGCAGTCCTGGAGACCAACA 2203
Db	2110	ACGCCCTTAACCGACGGTCTCCCAAGATCGCGCAATCGCACGGCAGTCCTGGAGACCAACA 2169
Qy	2204	CGGCCGTAGCCGAGGGCTATGGCTTATTCTGGTGAATCTCTGATCCAAATGAAAAGC 2263
Db	2170	CGGCCGTAGCCGAGGGCTATGGCTTATTCTGGTGAATCTCTGATCCAAATGAAAAGC 2229
Qy	2264	TCTACACCCCTGGATTACTACCTAAAGATGGCAGGGAGATCGTCAAGTCTGGGCTCACA 2323
Db	2230	TCTACACCCCTGGATTACTACCTAAAGATGGCAGGGAGATCGTCAAGTCTGGGCTCACA 2289
Qy	2324	TCTTGGCCATTAAAGGATAAGCTGGCTCTGGGCAACCCACGGACACTGGGGTCA 2383
Db	2290	TCTTGGCCATTAAAGGATAAGCTGGCTGGTCTGGGCAACCCACGGACACTGGGGTCA 2349
Qy	2384	CGGCAACTGGGCAACCTACTTGTGCAAGCTGGCTCAGTGCACGGTCTGGGGTCA 2443
Db	2410	CGGCAACTGGGCAACCTACTTGTGCAAGCTGGCTCAGTGCACGGTCTGGGGTCA 2469
Qy	2504	CGGCAACCTGCTGGCACACCTCCAGGCCATTCCCTGTGCAATTGTTGCTGCAT 2563

Db	2470	CCGCACCCACTGCTGGCACCCACTCCCAGCCATCCCTGTCTGCCATTCCCTGCTGATTGCTTCG 2529
Qy	2564	CGCACACCGTCCGATACCGGTTGAGCCTCGAGGCTCTGTTCTGACCTCGAGGCCGCTACT 2623
Db	2530	CGCACACCCGTGCGATACCGGTTGAGCCTCGAGGCTCTGTTCTGACCTCGAGGCCGCTACT 2589
Qy	2624	GGGAAGCAACTGTGCGGAACTGTACCTGCCATTGGAGTCTGAAACCCAGGGCAACCGGTC 2683
Db	2590	GGGAAGCAACTGTGCGGAACTGTACCTGCCATTGGAGTCTGAAACCCAGGGCAACCGGTC 2649
Qy	2684	GCGTCTACCGCACGAATCCAGGGGACAGTGTCCAACCTGCGTGCACAGGCCACCG 2743
Db	2650	GCGTCTACGGCACGAATCCAGGGGACAGTGTCCAACCTGCGTGCACAGGCCACCG 2709
Qy	2744	CACTGGCCTTGCGGATCGTTGAACTCATCGAAGACAACCTAGCAGGCCGTTAATGAGA 2803
Db	2710	CACTGGCCTTGCGGATCGTTGAACTCATCGAAGACAACCTAGCAGGCCGTTAATGAGA 2769
Qy	2804	TGCTGGGACGCCAACCAAGGTCACCCCATCCTCCAAAGGTTGTTGGGACCTCGCACTCC 2863
Db	2770	TGCTGGGACGCCAACCAAGGTCACCCCATCCTCCAAAGGTTGTTGGGACCTCGCACTCC 2829
Qy	2864	ACCTCGTTGGGTTGCTGGGAGACTTGTGGATCCAGCAGACTTGTGGCTGCCGATCCACAAAAGTAGCACA 2923
Db	2830	ACCTCGTTGGGATCCAGCAGACTTGTGGCTGCCGAGCTTGTGGTAACCCCTGCCGATCCACAAAAGTAGCACA 2889
Qy	2924	TCCCAGACTCTGTCATGGCTTCTGGGATCCAGCAGACTTGTGGTAACCCCTGCCGATCCACAAAAGTAGCACA 2983
Db	2890	TCCCAGACTCTGTCATGGCTTCTGGGATCCAGCAGACTTGTGGTAACCCCTGCCGATCCACAAAAGTAGCACA 2949
Qy	2984	CAGAGCCACTGGCACCCGGCACTGGAAAGGCCAAGGGCAACCTCTGACGG 3043
Db	2950	CAGAGCCACTGGCACCCGGCACTGGAAAGGCCAAGGGCAACCTCTGACGG 3009
Qy	3044	AAGTTCTGAGGAAGGCCAGGGCCACCTCGACGGCTGATGATTCCAAGGAACCGTCCGAAATA 3103
Db	3010	AAGTTCTGAGGAAGGCCAGGGCACCTCGACGGCTGATGATTCCAAGGAACCGTCCGAAATA 3069
Qy	3104	GCCTCAACCGCCTGCTGGGAAAGAGGTTCCCTCGAGCACCCGTCGCCGCT 3163
Db	3070	GCCTCAACCGCCTGCTGGGAAAGAGGTTCCCTCGAGCACCCGTCGCCGCT 3129
Qy	3164	TGGCAACACCCCTGCTGGGATGATCGTAATTCTTCTACGGCCTGGATGGCGCG 3223
Db	3130	TCGGCAACACCCCTGCTGGGATGATCGTAATTCTTCTACGGCCTGGATGGCGCG 3189
Qy	3224	AGACTTTGATCCGCCTGCCAGATGTGGCTGCCACCCACTGCCAGATGCCGATCT 3283
Db	3190	AGACTTTGATCCGCCTGCCAGATGTGGCTGCCACCCACTGCCAGATGCCGATCT 3249
Qy	3284	CTGAGCCAGACGATAAGGGTATGGCAATGTTGGCCAAACGTCACGGCCAGATCCGCC 3343
Db	3250	CTGAGCCAGACGATAAGGGTATGGCAATGTTGGCCAAACGTCACGGCCAGATCCGCC 3309
Qy	3344	CAATGCGTGTGCGTGAACCGCTCGTTGAGTCTGTCACCCGAAACGGCAGATT 3403
Db	3310	CAATGCGTGTGCGTGAACCGCTCGTTGAGTCTGTCACCCGAAACGGCAGATT 3369
Qy	3404	CCTCCAACAAGGCCATGTTGCTGCCACCATCGCTGGTGTGACTGTGTGCTG 3463
Db	3370	CCTCCAACAAGGCCATGTTGCTGCCACCATCGCTGGTGTGACTGTGTGCTG 3429
Qy	3464	AAGGTGATGAGGTCAAGGCTGGAGATGCGACTCGCAATTATCGAGGCCATGGAAAG 3523
Db	3430	AAGGTGATGAGGTCAAGGCTGGAGATGCGACTCGCAATTATCGAGGCCATGGAAAG 3489
Qy	3524	CAACAAATCACTGCTTGTGAGCAAAATGGATGGCTTCCTGCTGCAACGA 3583
Db	3490	CAACAAATCACTGCTTGTGAGCAAAATGGATGGCTTCCTGCTGCAACGA 3549
Qy	3584	AGGTGGAAGGGTGGGACCTGATCGTCGTTCCCTAA 3621
Db	3550	AGGTGGAAGGGTGGGACCTGATCGTCGTTCCCTAA 3587

1261	GCTGAGTTCAACCGTGTCTGGTGTCTGGAAACCAACATGGTTCTGGGTGTTCTGGCTGGGG 1320
1519	GAAGAGGACTTCACTTCCAAGGGCATGCCAACGGATTCAATTGGGATTCACCCGCACCTC 1578
1321	GAAGAGGACTTCACTTCCAAGGGCATGCCAACGGATTCAATTGGGATTCACCCGCACCTC 1380
1579	CTTCAGGCTCCACCTGCTGATGAGCAGGGACCCATCCTGGATTACTITGGCAGAATGTC 1638
1381	CTTCAGGCTCCACCTGCTGATGAGCAGGGACCCATCCTGGATTACTITGGCAGAATGTC 1440
1639	ACCGTGAACAAAGCCTCATGGTGTCCAAAGGGATGTTGGCAGCTCCTATCGATAAGCTG 1698
1441	ACCGTGAACAAAGCCTCATGGTGTCCAAAGGGATGTTGGCAGCTCCTATCGATAAGCTG 1500
1699	CCTAACATCAAGGATCTGCCACTGCCAACGGGTTCCCGTGACCGGCCCTGAGCGCTTGGC 1758
1501	CCTAACATCAAGGATCTGCCACTGCCAACGGGTTCCCGTGACCGGCCCTGAGCGCTTGGC 1560
1759	CCAGGCCGGTTTGCTCGTGAATCTCCGTGAGCAGGACGGCACTGGCAGTTACTGATAACC 1818
1561	CCAGGCCGGTTTGCTCGTGAATCTCCGTGAGCAGGACGGCACTGGCAGTTACTGATAACC 1620
1819	TTCGGCGATGCCAACCAAGTCTTGCTTGCACCCGAGTCCGCTCATTGGCACTGAAGCCT 1878
1621	TTCGGCGATGCCAACCAAGTCTTGCTTGCACCCGAGTCCGCTCATTGGCACTGAAGCCT 1680
1879	GGGGCAAGGGCCGTGCAAAGGTGACTCCTGAGCTTCTTGTCCGTGGGACAGGGCTGACCGAG 1938
1681	GGGGCAAGGGCCGTGCAAAGGTGACTCCTGAGCTTCTTGTCCGTGGGACAGGGCTGACCGAG 1740
1939	GCGACACTACGATGTGGGATGCGTTTCTCTTGAGGATCCGGTGGGACAGGGCTGACCGAG 1998
1741	GCGACACTACGATGTGGGATGCGTTTCTCTTGAGGATCCGGTGGGACAGGGCTGACCGAG 1800
1999	CTGGCGAGGGGATGCCGAATGTAACATTCAGATGCTGCTTGGGCCAACACCCGTG 2058
1801	CTGGCGAGGGGATGCCGAATGTAACATTCAGATGCTGCTTGGGCCAACACCCGTG 1860
2059	GGATACACCCGTACCCAGACTCCGGCTGCGCGGTTTGTGTTAAGGAAGCTGGCAGCTCC 2118
1861	GGATACACCCGTACCCAGACTCCGGCTGCGCGGTTTGTGTTAAGGAAGCTGGCAGCTCC 1920
2119	GGCGTGGACATCTTCCGCATCTTGACGGCTTAACGACGTCTCCAGATGGTCCAGCA 2178
1921	GGCGTGGACATCTTCCGCATCTTGACGGCTTAACGACGTCTCCAGATGGTCCAGCA 1980
2179	ATCGACGGCAGTCTGGGAAACCCGGTAGGCCAACTGGCTTATGGCTTATCTGGT 2238
1981	ATCGACGGCAGTCTGGGAAACCCGGTAGGCCAACTGGCTTATGGCTTATCTGGT 2040
2239	GATCTCTCTGATCCAATGAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGAG 2298
2041	GATCTCTCTGATCCAATGAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGAG 2100
2299	GAGATCGTCAAGTCTGGCTCACATCTGGCATTAAAGGATATGGCTTGGCTTCGGC 2358
2101	GAGATCGTCAAGTCTGGCTCACATCTGGCATTAAAGGATATGGCTTGGCTTCGGC 2160
2359	CCAGCTGGTAACCAAGCTGGTCACTGGCAACTGGCTGGTAATTCGATCTGGCTTCGGC 2418
2161	CCAGCTGGTAACCAAGCTGGTCACTGGCAACTGGCTGGTAATTCGATCTGGCTTCGGC 2220
2419	GTGCACACCCACGACACTTGCGGGTGGCCAAACCTACTTTGCTTGAGCTCAAGCT 2478
2221	GTGCACACCCACGACACTTGCGGGTGGCCAAACCTACTTTGCTTGAGCTCAAGCT 2280
2479	GGTGCAGATGGTGAACGGTCTGGGTTGGCTGGGATACGGGTTGGCTCGAGCTCGAG 2598
2281	GGTGCAGATGGTGAACGGTCTGGGTTGGCTGGGATACGGGTTGGCTCGAGCTCGAG 2400
2539	CTGTCTGCCATTGGTGTGCAATTGGGCAACCCGGTCCGATACGGGTTGGCTCGAG 2538
2341	CTGTCTGCCATTGGTGTGCAATTGGGCAACCCGGTCCGATACGGGTTGGCTCGAG 2400

RESULT 8
ABK52832
ID ABK

XX ABK52832;

XX 27-AUG-2002 (first entry)

XX Corynebacterium glutamicum feedback-resistant pyruvate carboxylase gene.

XX Feedback-resistant; pyruvate carboxylase enzyme; gene; db;

KW aspartic acid feedback inhibition resistant.

XX Corynebacterium glutamicum.

XX Key Location/Qualifiers

 1. .3474

 /* tag= a

 product= "Corynebacterium glutamicum feedback-resistant

 pyruvate carboxylase enzyme"

 /transl_except= (pos:1..3; aa:Met)

XX WO200231158-A2.

XX 12-OCT-2001; 2001WO-US031893.

PP 13-OCT-2000; 2000US-0239913P.

XX (ARCH) ARCHER-DANIELS MIDLAND CO.

XX Hanke PD;

XX WPI; 2002-463267/49.

DR P-PSDB; AAU98050.

XX Novel mutated, feedback resistant pyruvate carboxylase enzyme polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.

XX (ARCH) ARCHER-DANIELS MIDLAND CO.

PS Claim 3; Fig 1; 42pp; English.

XX The present invention relates to a new mutated, feedback-resistant pyruvate carboxylase enzyme. The invention is useful for producing an amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by culturing a host cell in a suitable media and separating the amino acid from the medium. The vector of the invention is useful for replacement of a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic copy of the wild-type pyruvate carboxylase gene with a selectable marker gene through homologous recombination to form a first recombinant strain, and replacing the selectable marker gene in the first recombinant strain, with feedback resistant pyruvate carboxylase gene through homologous recombination to form a second recombinant strain, where the homologous recombination in the above steps, occurs between the host cell and the vector. The feedback-resistant pyruvate carboxylase enzyme is resistant to feedback inhibition from aspartic acid. The present nucleic acid sequence encodes the feedback-resistant pyruvate carboxylase enzyme of the invention.

XX Sequence 3474 BP; 749 A; 1013 C; 950 G; 762 T; 0 U; 0 Other;

Query Match 93.9%; Score 3398.8; DB 6; Length 3474;

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 47; Indels 0; Gaps 0;

Matches 3427; Conservative 0;

Qy 148 GTGACTGCATCACCCRTGGGGTCTTGTGAAAGGAATAATTACTCTAGTGTGCACT 207

 1 GTGACTGCATCACCCRTGGGGTCTTGTGAAAGGAATAATTACTCTAGTGTGCACT 60

Db 208 CACACATCTAACGTTCCAGGATTCAAAAAGATCTTGTGAAAGGAATAATTACTCTAGTGTGCACT 267

 61 CACACATCTAACGTTCCAGGATTCAAAAAGATCTTGTGAAAGGAATAATTACTCTAGTGTGCACT 120

Qy 268 GCGGTCGGTGGGGAAATCACCGCACACTCGTGGCACGCCAACGGTGGCACGCCAACGGTGGCAC 1347

 1348 GCGGCTCAGCTGGGGAAATCACCGCACACTCGTGGCACGCCAACGGTGGCACGCCAACGGTGGCAC 1407

Db 121 GCGTCCTGGCTTCCGTGAGCACTCGAACCCGGTGGCAGCCACGGTAGCTATTACCCC 180

Qy 328 CGTGAAGATCGGGATCATTCACCGCTCTTGTGAAGCTGTGGCATGGTACCT 387

Db 181 CGTGAAGATCGGGATCATTCACCGCTCTTGTGAAGCTGTGGCATGGTACT 240

XX GAAGGCTCACCAAGTCAGGCTACCTGGACATCGATGAATTATCGGTGAGCTAAAGAA 447

KW KW

XX GAAGGCTCACCAAGTCAGGCTACCTGGACATCGATGAATTATCGGTGAGCTAAAGAA 300

OS OS

XX

FH Key

CDS /* tag= a

FT product= "Corynebacterium glutamicum feedback-resistant

FT pyruvate carboxylase enzyme"

FT /transl_except= (pos:1..3; aa:Met)

XX

PN PN

XX 18-APR-2002.

XX 421 ACCGGTGATAAGTCTGCCGGTAACGCCGGCAAGAAGGGCTGGCTGCCAGTTGGCG 627

PP 421 ACCGGTGATAAGTCTGCCGGTAACGCCGGCAAGAAGGGCTGGCTGCCAGTTGGCG 480

DB 421 ACCGGTGATAAGTCTGCCGGTAACGCCGGCAAGAAGGGCTGGCTGCCAGTTGGCG 540

QY 628 GAATCCACCCCGAGCAAACATCGATGAGATCGTTAAAGGGCTGAAGGCCAGACTTAC 687

DB 481 GAATCCACCCCGAGCAAACATCGATGACATCGTTAAAGGCCAGACTTAC 540

QY 628 CCTGATCTTGTGAGGCCAGTTGCCGGTGTGGCCGACGGGTATGCCGTGTTCTTCA 747

DB 541 CCCATCTTGTAAAGGCAAGTTGCCGGTGTGGCCGACGGGTATGCCGTGTTCTTCA 600

QY 748 CCTGATGAGGCTCGCAAAATTAGCAACGAAGGATCTCGTGAAGCTGAAGGGCTTTCGGC 807

DB 601 CCTGATGAGGCTCGCAAAATTGGCAACGAAGGATCTCGTGAAGCTGAAGGGCTTTCGGC 660

QY 808 GATGGCGGGTATATGTCGAAACGCTGATTAAACCTCAGGCAATTGAAAGTGCAGATC 867

DB 661 GACGGTTCGGTATATGTCGAAACGCTGATTAAACCCGACATGGCATTCGGCATTGGC 720

QY 868 CTGGGGATCACACTGGAGAAGTTGACACCTTATGAAACGTGACTGCTCACTGCAGCGT 927

DB 721 CTGGGGATCGACTGGAGAAGTTGACACCTTATGAAACGTGACTGCTCACTGCAGCGT 780

QY 928 CGTACCAAAAGTTGTCGAAATTCGCCCCACGCAAGCATTGGATCCAGAACCTGGTGT 987

DB 781 CGTACCAAAAGTTGTCGAAATTCGCCCCACGCAAGCATTGGATCCAGAACCTGGTGT 840

QY 988 CGCATTTGGGGATGGCAAGTTGCTGCGTCCATTGGTACCGGGGGAAACC 1047

DB 841 CGCATTTGGGGATGGCAAGTTGCTGCGTCCATTGGTACCGGGGGAAACC 900

QY 1048 GTGGAATTCTGGTGGTCAATGGAAACCCACGTATCGAAATGAACCCACGTATC 1107

DB 901 GTGGAATTCTGGTGGTCAATGGAAACCCACGTATCGAAATGAACCCACGTATC 960

QY 1108 CAGGTTGAGCACACCGTGAAGAAGTCACCGGAGGTGGACCTGGTGAAGGGCAGATG 1167

DB 961 CAGGTTGAGCACACCGTGAAGAAGTCACCGGAGGTGGACCTGGTGAAGGGCAGATG 1020

QY 1168 CGCTTGGTGGCTGCAACCTTGTGAAAGGAATTGGGTCTGACCCAAGATAAGTCAAGACC 1227

DB 1021 CGCTTGGTGGCTGCAACCTTGTGAAAGGAATTGGGTCTGACCCAAGATAAGTCAAGACC 1080

QY 1228 CACGGTGGAGACTCGAGTGCCTCACCCAGGATCCAAACAAACGGCTTCCGCCCA 1287

DB 1081 CACGGTGGAGACTCGAGTGCCTCACCCAGGATCCAAACAAACGGCTTCCGCCCA 1140

QY 1288 GATACCGGAACATCACCGGCTACCGGCTTGGGGTGGCTGTTGTGACGGT 1347

DB 1141 GATACCGGAACATCACCGGCTACCGGCTTGGGGTGGCTGTTGTGACGGT 1200

QY 1348 GCGGCTCAGCTGGGGAAATCACCGCACACTCGTGGCACGCCAACGGTGGCACGCCAACGGTGGCAC 1407

Db	1201	GGAGCTCAGCTCGGGGAAATCACCGCAACTTGTACTCCATGGTGAATAATGACC	1260		
QY	1408	TGCCGTGGTTCCGACTTTGAAACACTGCTGTTGCAAGGGCCTGGCTGAGTC	1467	QY	2488 GCTGTTGACGGTGCTTCCGACCACTGCTGCTGGCAACCCCTCCAGGCCATTCCCTGTCGCCC 2547
Db	1261	TGCCGTGGTTCCGACTTTGAAACTGCTGTTGCAAGGGCCTGGCTGAGTC	1320	Db	2341 GCTGTTGACGGTGCTTCCGACCACTGCTGCTGGCAACCCCTCCAGGCCATTCCCTGTCGCCC 2400
QY	1468	ACCGTGTCTGGGTGCAACCAAATGGTTTCTGCGTGGCTGGAAAGGGAC	1527	QY	2548 ATGGTGTGCTGCAATTGGGCAACCCGGTGGGATACCGGTTTGAGGCTGAGGCTGAGTTCT 2607
Db	1321	ACCGTGTCTGGGTGCAACCAAATGGTTTCTGCGTGGCTGGAAAGGGAC	1380	Db	2401 ATGGTGTGCTGCAATTGGGCAACCCGGTGGGATACCGGTTTGAGGCTGAGTTCT 2460
QY	1528	TTCACCTCCAGGGCATGGGATTCAATTGGGATCACCGCACCTCTTCAGGCT	1587	QY	2608 GACCTGAGGGTACTGGGAAGCAGTGTACCTGCCATTGAGTCATGGCAACCCTG 2667
Db	1381	TTCACCTCCAGGGCATGGGATTCAACCTCTTCAGGCT	1440	Db	2461 GACCTGAGGGTACTGGGAAGCAGTGTACCTGCCATTGAGTCATGGCAACCCTG 2520
QY	1588	CCACCTGTGTGATGATGAGGGGAGGCATCTGGGATACTGGCAATGGTACCGTGAAAC	1647	QY	2668 CCAGGCCAACCGGGTGGCTTACCGGCCACGAAATCCAGGGACAGTTGTCACCTG 2727
Db	1441	CCACCTGCGGATGATGAGGGGAGGCATCTGGGATACCGTGAAAC	1500	Db	2521 CCAGGCCAACCGGTGGCTTACCGGCCACGAAATCCAGGGACAGTTGTCACCTG 2580
QY	1648	AAGCCTCAGTGTGCTCCAAGGGATGTTGAGCTCTGGATAAGCTGCTAACATC	1707	QY	2728 CGTGACAGGCCACCGCACTGGCCTTGCAGCTCATGAAAGACAATC 2787
Db	1501	AAGCCTCAGTGTGCTCCAAGGGATGTTGAGCTAACATGATAAGCTAACATC	1560	Db	2581 CGTGACAGGCCACCGCACTGGCCTTGCAGCTCATGAAAGACAATC 2640
QY	1708	AAGGATCTGCAACTGCCACTGGGTTCCCGTGAACGGCTGGGAGCTGGCG	1767	QY	2788 GCAGCCGTTAATGAGATGTTGAGCTGGGAGCCAAAGGTCACCCCATCTCCAAAGGGTT 2847
Db	1561	AAGGATCTGCAACTGCCACTGGGTTCCCGTGAACGGCTGGGAGCTGGCG	1620	Db	2641 GCAGCCGTTAATGAGATGTTGAGCTGGGAGCCAAAGGTCACCCCATCTCCAAAGGGTT 2700
QY	1768	TTTGCTCGTGAATCTCGTGAACGGGACTGGCACTGGCACTGGCACTGGGAGCTGGCG	1827	QY	2848 GGCGACCTGCACTCCACCTCGTTGCTGGGATTCAGCAGACTTTGCTGCCGAT 2907
Db	1621	TTTGCTCGTGAATCTCGTGAACGGGACTGGCACTGGCACTGGGAGCTGGCG	1680	Db	2701 GCGGACCTGCACTCCACCTGGCACTGGCACTGGGAGCTTAGTCAGCAGAC 2760
QY	1828	GCACACCGTCTGGCTGACTCCTGAGCTGGCACTGGCACTGGCACTGGGAG	1887	QY	2908 CCACAAAGTAGCACTCCAGACTCTGCTGATCGCTGCTGGGAGCTGGTAAC 2967
Db	1681	GCACACCGTCTGGCTTGGCAACCCGGACTGTCGACTGAAGGCTGGCAAGAG	1740	Db	2761 CCACAAAGTAGCACTCCAGACTCTGCTGATCGCTGCTGGGAGCTGGTAAC 2820
QY	1888	GCGCTGGCAAGGCTGAGCTGGCTTGTGAGCTGGCACTGGCACTGGGAGCTAC	1947	QY	2968 CCTCCAGGTGGCTGGCAAGGCCACTGGCACTGGCACTGGCACTGGGAG 3027
Db	1741	GCGCTGGCAAGGCTGAGCTGGCACTGGCACTGGCACTGGCACTGGCACTAC	1800	Db	2821 CCTCCAGGTGGCTGGCAAGAACCTGGCAACCCGCACTGGCACTGGGAG 2880
QY	1948	GATGTTGGCATGGTAAACATTGAGATGGCTTGGGAGCTGGCAACACCTGGGAG	2007	QY	3028 AAGGCACCTCTGACGGAAAGTTCTCTGAGGAAGGAGCAAGGGCAACCTG 3087
Db	1801	GATGTTGGCATGGTTCCTCTGGGAGCTGGCAACACCTGGGAGCTGGGAG	1860	Db	2881 AAGGCAACCTCTGACGGAAAGTTCTCTGAGGAAGGAGCAACCCGCAACCTG 2940
QY	2008	GCGATGCCGAATGTAACATTGAGATGGCTTGGGAGCTGGCAACACCTGGGAG	2067	QY	3088 AAGGAACGTCGCAATAGCTCAACGGCTCTGCTGTTCCGAACCGAAAGAGTCCTC 3147
Db	1861	GCGATGCCGAATGTAACATTGAGATGGCTTGGGAGCTGGGAGCTGGGAG	1920	Db	2941 AAGGAACGTCGCAACAGGCTCAACGGCTCAGGACTTCGCTGATGATTCC 3000
QY	2068	CCGTACCCAGACTCCGCTGGGGGGGAAACACCGTGGGAGATAACC	2127	QY	3148 GAGCACCGTCGGGCTTGGCAACACCCCTCTGCGTGGATGATGTTCTACGGC 3207
Db	1921	CCGTACCCAGACTCCGCTGGGGGGGAAACACCGTGGGAGATAACC	1980	Db	3001 GAGCACCGTCGGGCTTGGCAACACCCCTCTGCGTGGATGATGTTCTACGGC 3060
QY	2128	ATCTTCGGCATCTGAGCGGCTTAACGAGCTCCAGATGGTCCAGCAATCGACGCA	2187	QY	3208 CTGTCGAAAGCCGAGCTCTGAGCCAGTTGCTGCGCACCCACTGCTGTTGTT 3267
Db	1981	ATCTTCGGCATCTGAGCGGCTTAACGAGCTCCAGATGGTCCAGCAATCGACGCA	2040	Db	3061 CTGTCGAAAGCCGAGACTTGTGCTGCGCACCTGCTGCGAGATGTTGTTGTT 3120
QY	2188	GTCCTGGAGACCAAACACCGGGTAGCCAGGGCTATGGCTTATCTGGTGAATCTCT	2247	QY	3268 CGCTCTGGATGCGGATCTGAGCCAGGATAAGGTTATGGCAATGTTGTTGCCAACGTC 3327
Db	2041	GTCCTGGAGACCAAACACCGGGTAGCCAGGGCTATGGCTTATCTGGTGAATCTCT	2100	Db	3121 CGCTGGATGCGGATCTGAGCCAGGATAAGGTTATGGCAATGTTGTTGCCAACGTC 3180
QY	2248	GATCCAAATGAAAAGCTCTAACCCCTGGGATTAAGCTTAAGATGGCAAGGGAGATCGTC	2307	QY	3328 AACGGCCAGATCCGCCAATGGCTGAGCTGGGCAACCTGCTGAGCTGGCTGAGCTGGCAAC 3387
Db	2101	GATCCAAATGAAAAGCTCTAACCCCTGGGATTAAGCTTAAGATGGCAAGGGAGATCGTC	2160	Db	3181 AACGGCCAGATCCGCCAATGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCAAC 3240
QY	2308	AAGTCTGGCTCACATCTGGCCATTAAAGGATATGGCTGGCTCTGCTGAGCTGGCT	2367	QY	3388 GCAGAAAAGGAGATGGAAGGCAACCTGCTGAGCTGGCAACCTGATCGCTGTTGTC 3447
Db	2161	AAGTCTGGGCTCACATTCTGGCCATTAAAGGATATGGCTGGCTCTGCTGAGCTGGCT	2220	Db	3241 GCAGAAAAGGAGATGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCAAC 3300
QY	2221	GTAACCAAGTGGTCAACGGCACTGGGGCAAGTGGCTGAGCTGGCAAC	2280	QY	3448 ACCGTGACTGTTGCTGAGCTGGCAACCTGATCGCTGTTGTC 3507
Db	2281	CACGACACCTGGGGCAAGCTGGCAACCTACRTGGCTGCAAGCTGGCTACCTTGTGCAAGCTGGCAAGAT	2340	Db	3301 ACTGTGACTGTTGCTGAGCTGGCTGAGCTGGCTGAGCTGGCAAC 3360

Qy 3568 GTTCTGTCACGAAAGGTGGAAAGGTGGCAACTTGATCGTCGTTCCCAAAGGCTGGTCAACGCTTCAACGATCAGCTGGTCTCGTGAAG 3621
 Db 3421 GRTCCRGTGCAACGAAAGGTGGAAAGGTGGCAACTTGATCGTCGTTCCCAAAGGCTGGTCAACGCTTCAACGATCAGCTGGTCTCGTGAAG 3474

RESULT 9
AAF87437 ID AAF87437 standard; DNA; 4013 BP.
 XX AC AAF87437;
 XX DT 09-JUL-2001 (First entry)
 DE Corynebacterium thermoaminogenes pc nucleotide sequence.
 XX KW Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
 KW thermotolerant; aceA; accBC; dtSR1; dtSR2; pfk; scrB; gluABCD; pdhA; pc;
 ppc; acn; icd; lpd; odhA; ds.
 XX OS Corynebacterium thermoaminogenes.
 XX FH Key Location/Qualifiers
 CDS 319 .3738 /*tag= a
 FT product= "pc protein"
 FT PN WO200125447-A1.
 XX PD 12-APR-2001.
 XX PF 04-OCT-2000; 2000WO-JP0006913.
 XX PR 04-OCT-1999; 99JP-00282716.
 PR 01-NOV-1999; 99JP-00311147.
 PR 21-APR-2000; 2000JP-00120687.
 XX PA (AJIN) AJINOMOTO CO INC.
 PI Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K,
 PI Kimura E, Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
 PI Sugimoto S;
 XX DR P-2001-300170/31.
 DR P-PSDB; AAB83180.
 XX PT Proteins and their DNA useful for microbial production of L-amino acids.
 XX PS Claim 34; Page 126-132; 215pp; Japanese.
 XX CC The present sequence is provided in a specificaion relating to genes
 CC encoding thermophilic amino acid biosynthesis system enzymes of the
 CC thermotolerant bacterium Corynebacterium thermoaminogenes. The novel
 CC proteins retain at least 30% isocitrate ligase activity after heating at
 CC 500C for 5 minutes. DNA fragments encoding the enzymes were isolated from
 CC a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by
 CC PCR. The DNA may be used for developing strains of amino acid producing
 CC microorganisms
 XX SQ Sequence 4013 BP; 735 A; 1376 C; 1234 G; 668 T; 0 U; 0 Other;

Query Match 63.0%; Score 2279.6; DB 5; Length 4013;
 Best Local Similarity 77.7%; Pred. No. 0; Mismatches 799; Indels 9; Gaps 4;
 Matches 2808; Conservative 0; Gaps 4;

Qy 7 GGGTTAGATCCTGGGGTTTATTCACTTGAAGTGTGCAGGTCAAGGG 66
 Db 129 GGGTCTGGGGCATTCAGGCAAGGGTCACTC 188

Qy 67 GAGTGTGCCAAAACATTGAGAGAAAACAAAACCGATGTTGATGGGAAATCGG 126
 Db 189 CCCGCCGGGTAGAGAACGGGAAAGGAATACTGGTTTCCGGACTGG 248

Qy 127 GGTTACGATACTAGGACGCACTGACTGCTATCACCCCTT-GGCGTCTCTGGTAAAG 184

Qy 1025 TTGGTTACCGGCCGAGCTGGCGATGCCGATCTGTGCAAAATCCA 1144
 Db 1145 TCGATACCGGGCGACCTTGTGAGTTCTCGTCAACCACGGTCT 1204

Qy 1085 TCATCGAAATGAAACCCACGTATCCAGGTGACTGAAGAAGTCACCGGAGG 1144
 Db 1205 TCATTGAGATGAAACCCCGCATCCAGGTGACACCCGTGAGGAGTCACCTCCG 1264

Qy 1145 TGGACCTGGTAAGGGCGAGATGCTGGTGGTGAACCTTGAAGGAATTGGTC 1204
 Db 1265 TCGACCTGGTCAAGGGCGAGATGCACTGGCCACCTGGTGAAGGAACCTGGCC 1324

Qy 1205 TGACCCAAAGATAAGATCAAGACCCACGGTCACTGAGTGCAGTCAACCCTT-GGCGTCTCTGGTAAAG 1264

Db	1325	TGACCCAGGACAAGATCACCCACGGTCCCCCTGGACTCACCGGAGG	1384
Qy	1265	ATCCAAACAACGGCTTCCGCCAGATAACCGAACTATCACCGTACCCAGGGG	1324
Db	1385	ACCGTCAAACTTCCGGCCGACACGGGTGTGATCACCGCTTACCGCTCCCCGGTG	1444
Qy	1325	GAGCTGGGTTCTGTTGACGGTGCAGTCAGCTGGGAATTACCGCACACTTGG	1384
Db	1445	GTGGGGGTTGCTGCTGACGGCAGCTGGGGAGATCACCGCACATTTCG	1504
Qy	1385	ACTCCATGCTGTGAAATTGACTCTGGCTGGTTCCGACTTGTGCTCGTG	1444
Db	1505	ATTCATGCTGGTCAAGATGACTGCGGGTTCCGATTTGCTCCGAG	1564
Qy	1445	CACAGGGGGTTGACTGGCTGAGTTACCGTGTGGTCAACCAACTTGGTTC	1504
Db	1565	CCAGGGCCCTGGGGAGTTAACGTCTCCGGTACATGGCTTCCCTGC	1624
Qy	1505	GTGGCTTGTGCTGGGTTGAGCTTACCGTGTGGTCAACCAACTTGGTTC	1564
Db	1625	GTGGCTGCTGGTCAAGATGACTGCGGGTTAACGGCTTACGGCT	1684
Qy	1565	ATCACCCGACCTCTTCAAGGACTTCACTTCCAAGGCATCTGGT	1624
Db	1685	CCCACCAAGCACCTCTTCAAGGCTTCAAGGACTTCACTTCCAAGG	1744
Qy	1625	ACTTGGGAGATGTCACTGGTCAAGGCTCATGGTGTGGTCAAGGCC	1684
Db	1745	ACCTGGGGATGTCACCCGTGAAACAAAGGCTCATGGTGTGGTCAAGGCC	1801
Qy	1685	CTATCGATAAGCTGCTAACATCAAGGATCTGCCACTGGCAAGGCC	1744
Db	1802	CGATAGGAAGCTGGCCAGGGTGAAGAACAAACCCACGGTGAAGGCC	1861
Qy	1745	TGAAGCAGCTTGGCCAGGCCAGTGGTCAACCCGAGTGGCACTGGCAG	1804
Db	1862	TGAAGCAGCTGGCCGGGTTTCGCGGAGATCTGGCAACAGGATGCCCT	1921
Qy	1805	TTAAGTACACCTTCCGGATGCAACCCAGTCTTGGTCAACCCGAGTGGCTCAT	1864
Db	1922	TCACCGAACACCCTCCGGATGCCACCCAGTCCCTCTGGCAACCGGCT	1981
Qy	1865	TGCGACTGAAGCCTGGGGAGGGCCGCTGGGATGGTCAACGGGACTGG	1924
Db	1982	TCGGCTGACCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2041
Qy	1925	AGGGCTGG	1984
Db	2042	AGGCTGG	2101
Qy	1985	ACAGGGCTGACGAGCTGGGATGCCGAGTGGGATGCCGAGTGGGG	2044
Db	2102	CACGCCAACCGTGGATGAGCTGGTGGGATGCCGAAATGTAACATCC	2161
Qy	2045	GCGGCAAACACCGTGGGATAACCCAGACTCGTCTGGCGGTTGTTAACG	2104
Db	2162	GTGCCAACACCGTGGGATACCCAGACTCGTCTGGCGGTTGTTAACG	2221
Qy	2105	AAGCTGCTGGCTGGGATGCCGAACTCTTCCGGCATCTTCAACGACAT	2164
Db	2222	AGGCCGCAAGTCCGGTGGGATGCCGAACTCTTCCGGCATCTTCAACGACAT	2281
Qy	2165	AGATGCGTCCAGCAATCGACGCACTCTTCCGGCATCTTCAACGACAT	2224
Db	2282	AGATGCCGG	2341
Qy	2225	TGGCTTAACTCTGGTGAATCCAAATGAAAAGCTCTAACCCCTGGAT	2284
Db	2342	TGGCTTAACTCTGGTGAACCTGTCAATCCGGGAGGCTAACCCCTGGACT	2401
Qy	2285	TAAGATGGCAGAGGAGATGTCAGTCAGTCAGTCAGTCAGTCAGTC	2344
Db	2402	TGAACTGGGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2461
Qy	2345	CTGGTCTGCCAGCTGGCCAGCTGGCAAGCTGGCTGGTGAATTTCG	2404
Db	2462	CGGCCCTGCTGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2521
Qy	2405	ATCGCCAGTGCAGTGGGAACACCCAGACACTGCGGGCTGGCAACCT	2464
Db	2522	ACCTGCCCGTGCATGTCACCCACGCCAGACGCCAGACGCCAGAC	2581
Qy	2465	CTGCAAGTCAAGTGGTCAAGATGGTGGCAAGATGGTGGTGGACCCA	2524
Db	2582	CCGCCCAAGGCCAGATGCCCTCTGCCACCCCTGTCGGTACCCA	2641
Qy	2525	CCTCCAGGCCATCCCTGCTGCATGTTGCTGCATTTCGGCATACCG	2584
Db	2642	CCTCCAGGCCGCTGATGTCGGCTGCTGGTGGGGACTGTTGCG	2701
Qy	2585	GTTGAGGCCCTGAGGCTGTTCTGACACTCGGCTGACTGGGAAGG	2644
Db	2702	GCCTCAACCTTGCAGGCCAACTGGCTGGTCCGGGGACTGTTGCG	2761
Qy	2645	ACCTGCCATTGAGTCTGGTCAACCCAGGGTACTGGAGGGGGCT	2704
Db	2762	ACCTGCCGGTTGAATTCGGGACCCGGGACGGTGGTTAACGGGACT	2821
Qy	2705	CAGGGAGCACTGGTCACTGGTGGCACAGGCCACCGCACTGGGCT	2764
Db	2822	CGGGCGGTCAAGGTCTGGTCAACCTGGTGGTCACTGGTGGTCA	2881
Qy	2765	TGAAACTCATGAAAGACAACTAGCAGGCCAACTGGCCAAACCA	2824
Db	2882	TGAGGCTCATCGAGGACTACTAGCGAGGGGGATCTGGTGGTCA	2941
Qy	2825	TCACCCCATCTCCAGGTTGCTGGGACTCTGGGACTCTGCTGTC	2884
Db	2942	TCACCCCGTCTCCAGGTTGCTGGTCACTGCACTCTGGGACTCTG	3001
Qy	2885	ATCAGGAGACTTGTGCGGATCCAGAACCTGGGACTCTGCTGTC	2944
Db	3002	GCCCGGAGGATTGCGGCACTCTGGTGGGAGATTCGGTCACTGCC	3061
Qy	2945	TCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3004
Db	3062	TCCTCCGGGGAAACTCTGGGTTGGCTGGGGGGGGGGGGGGGGGG	3121
Qy	3005	CACTGGAAAGGCGCTCCAGGCAAGGGCACTCTGACGGAAAGGAGC	3124
Db	3122	CACTGGGGGTGCTCCAGGGTAATTCGGTGGGGGGGGGGGGGGGG	3181
Qy	3065	CGCACCTCGACGCTGATGTTCCAGGTAACGGCTCAACCCGCTG	3124
Db	3182	CCACCTGGTAATTCGGTGGGGGGGGGGGGGGGGGGGGGGGGGG	3241
Qy	3125	CGAAGCCAACCGAAAGGTTCTCGGACCCGGCTTGGGAAACACCT	3184
Db	3242	CGAAGGCCACGGAGTTCTTGGCAACCTCCGGCTGGGAAACACCT	3301
Qy	3185	ATGATCGTGAATTCTTCTACGGGCTGGTGAAGGGCAAGCTTGT	3244
Db	3302	ATGACCGGCAACCCGATGGTCTCTACGGGTTGAGGGGGGGGGGG	3361
Qy	3245	ATGTCGGCACCCACTGCTGGTGAAGGGCAAGCTTGTGCCAG	3304
Db	3362	GTGTCCACCCGATGGTCTCTACGGGTTGAGGGGGGGGGGGGGGG	3421
Qy	3305	TGCGCAATGTTGGCCCAAGCTGGTGAACGGCTGGGGGGGGGG	3364
Db	3422	TGCGCAACGTGGTCAACGTCAAGGGGGGGGGGGGGGGGGGGGG	3481
Qy	3365	CCGTTGAGTGTGTCACCGCAACCGCAAGGGCAAGTCTCCAA	3424
Db	3482	CCGTTGAGTGTGTCACCGGCCACCGGGAGGGAGGGAGGGAGGG	3541

Qy 3425 CTGGCACCATTGCTGGTGTGACTACCGTGATGAGGTGATGAGGTCAAGGCTG 3484
 Db 3542 CGGCACCATTGCCGTCGGTGTGACTACCGTGATGAGGTCAAGGCTG 3601
 Qy 3485 GAGATGGCACTCCGCAATCATCGAGCTATGAGATGGGAAACATCACTGGTTCTGGTG 3544
 Db 3602 GGGACGGCGTGGCATCATGGGCCATCATGGAGATGGGACCATCACGGCTGTG 3661
 Qy 3545 ACGGAAATAATCGATGCCATTGTTCTGCTGCAACGAAGGTGGGAGCTTGA 3604
 Db 3662 ACGGTGTCAATGACCGCGTGTGCCCCGCCACCAAGTCGAGGGGGGACCTCA 3721

Qy 3605 TCGTCGTTCCTA 3620
 Db 3722 TCGTGGTGTGTCTA 3737

RESULT 10

ACA29831 standard; DNA; 3423 BP.

XX ACA29831;

XX DT 19-JUN-2003 (first entry)

XX DE Prokaryotic essential gene #111488.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.

XX OS Corynebacterium diphtheriae.

XX EN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-03662699P.

XX PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL,

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,

XX DR WPI; 2003-029926/02.

DR P-PSDB; ABU25961.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 17701; 1766pp; English.

XX

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway; (8) required for proliferation, or that inhibits cellular proliferation or the biological identifying a gene required for cellular proliferation or its gene product lies

or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 3423 BP; 773 A; 1058 C; 912 G; 680 T; 0 U; 0 Other;

Query Match	53.2%	Score 1927.4;	DB 7;	Length 3423;
Best Local Similarity	73.4%	Pred. No. 0;	Indels 9;	Gaps 2;
Matches 2494;	Conservative 0;	Mismatches 896;	Indels 9;	Gaps 2;
Qy 213 ATCTCAACGCTTCAGCATTCAAAAGATCTTGGTAGCAAACGGGGAAATCGCGGT 272	Db 27 AACCTCTACGGTAATCCATTGTCAAAGATCCTCGTTGCTAACGTGCGGAGATGCCGT 86			
Qy 273 CCGTGCCTTCGGCTCGAGCACTCGAAACGGGTGACGGTAGCTATTACCCCGTGA 332	Db 87 GCGGAGCTTTCTGTGCGCCCTTGAACCGGTACTACCGTAGCTACCGTAACCGA 146			
Qy 333 AGATCGGGATCATTCACCGCTCTTGTGACGGCTACCGTACCGTAACAGCTAA 452	Db 147 AGACCGTAATTCTACCGATCGTTGCCTCTCATGGTAAAGCTGCTGAGCTGCGGG 206			
Qy 393 CTCACCACTGCAAGGGTACCTGGACATCGATGAATTATCGTGTGAGCTAAAGTTAA 207	Db 207 ATCTGGGTCAAGGGTACCTCGATATCGAGAAATCATCGAGAAATCATCGGG 266			
Qy 453 AGGAGATGCCATTACCCGGGATACGGCTTCTGCTGAAATGCCAGCTTGGCGGA 512	Db 267 TGCCGAGCCTTTACCCAGGCTACGGCTTCCGAAAACGCCCAAGCTTGGCTGTGA 326			
Qy 513 GRTGGGGAAAACGGCATACTTTATTGGCCAACCCAGAGGTCTGTGATCTCACCGG 572	Db 327 GTCGGCTGAAACGGCATAACCTCCATCACTGCTGGAGCTTACCGGG 386			
Qy 573 TGATAAGTCTCGGCCGTAACCGCCGGTAAAGGGCTGGTCCAGTTGGGGAAATC 632	Db 387 TGATAAAAGCAGTGTGTACCGCAGCACGCCAACCTTATCGGTTACCGCTGAGAC 446			
Qy 633 CACCCGGAGCAAAACATCGATGAGATCGTTAAAGGGCTGAAAGCTTACCCCAT 692	Db 447 AGAAGCAACAGACGATCCAAAGAACCTGCAAGGTGACCAAGGGGAGCTACCCGCT 506			
Qy 693 CTTTGTGAGGGAGTTGCCGGTGGTGGGGACGGGTATGCCATTGGTCTCACCTGA 752	Db 507 ATTGTCAAAAGCCGTRGTACCGCAGCACGCCAACCTTATCGGTTGGCCGGCATGCGTGA 566			
Qy 753 TGAGCTTCGCAAAATTAGCAACAGAACATCTGTGAAGCTTATGAACTGCTGATCTGG 812	Db 567 AACCTGAAAGCTAGGCAAGCCCTCCGGTGCAGCATTCGGGATGG 626			
Qy 813 CGGGTATATGTCGAAACGTGCTGTGATTAACCTCAAGCATATTGAAAGTGCAGATCCTGG 872	Db 627 CGAGTCTACGGCGAGGTGCAACATCACTCCAGCATATTGAGGTCAGATCCTGG 686			
Qy 873 CGATCACACTGGAGAAGTTGTACACCTTATGAACTGCTCACTGCAAGCTGTCGA 932	Db 687 TGACTCCGGTGGCAACATCATCCACCTGACGAGCTGCTGGTGGCAGGGTGGCCA 746			
Qy 933 CCAAAAGTTGTCGAAATGGCCAGCACGCAACTTGGGATCCAGAATCCAGGAT 992	Qy			

QY 3153 CGGTCGGCCTGGCAACACCTCTGGATGATCGCTGAATTCTTACGGCCTGGT 3212 PR 09-JUL-1999; 99DE-01032227.
 Db 2958 CCGCCGTCAGTTGGATACCACCAACTCGGTGACGCCAATTCTTACGGCCTCAA 3017 PR 09-JUL-1999; 99DE-01032230.
 QY 3213 CGAAGGCCGGAGACTTTGATCCGGCTGCCAGATGGTGGCACCCCCATGCTTGTCGCCT 3272 PR 09-JUL-1999; 99US-0143208P.
 Db 3018 AGAAGCAAAGAACGGTCATTCTGTAACGGAGACAGTAGCCTGGTCCCATGGTGGTCT 3077 PR 14-JUL-1999; 99DE-01032924.
 QY 3273 GATGGGATCTCTGAGCCAGACGATAAGGGTATGGGCAATGGTGGCCAACGTCAACGG 3332 PR 14-JUL-1999; 99DE-01032971.
 Db 3078 CGATGCCGTCGGCGAGCGAAAGGGCATGGCAACGTTGGTGCACGG 3137 PR 14-JUL-1999; 99DE-01033005.
 QY 3333 CGAGATCCCAATGGCTGCCGTCGGTGAACCGCTCCGGTGAAGTGTGTCAACGG 3392 PR 27-AUG-1999; 99DE-01040765.
 Db 3138 CGAGATTGCCCATCTCTGGTGTAGAGTCAGTGACGGTAGGTCAACGGCTGGTGGAA 3197 PR 31-AUG-1999; 99US-0151572P.
 QY 3393 AAGGGCAGATTCTCCAAAGGCCATGGTGTGCACCATTCGCTGGTGTGTCAACGGT 3452 PR 03-SEP-1999; 99DE-01042076.
 Db 3198 AAAGGCTGATCTCCAAAGGGGACAGCTGGCAACGGTGTGTCAACAGT 3257 PA (BADI) BASF AG.
 QY 3453 GACTGGTGGCTGAAGGTGATGAGGTCAAGGCTGGAGATGGCAGTCGCAATCGAGGTAT 3512 XX PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 Db 3258 GACAATCGAGGAAGGGCTACCGTCAAAGGGCGATCAGTTGGTGTCAATTGAGGCAAT 3317 XX WPI; 2001-061975/07.
 QY 3513 GAAGATGGAAACAAATCAACTGCTTCAGGCTGGAGATGGCAGTCGCAATCGAGGTAT 3572 PT P-PSDB; AAB79302.
 Db 3318 GAAGATGGGGCAACGGATCTCTGCCACACAGACGGAAACCGTGAACCGTGTCTTGAC 3377 XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 metabolism and oxidative phosphorylation protein for production or
 modulation of production of fine chemicals e.g. amino acids.
 QY 3573 TGCTGCAAGGAAGGTGGAAGGTGGGACTTGATCGTCGT 3611 PS Claim 3; Page 316-319; 1246pp; English.
 Db 3378 GCAGGCCAACGTCAGGTGAAAGGTGGAGACTTGCTCCCTCGT 3416 XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
 to AAB 79633 which are involved in carbon metabolism and energy
 production. The C. glutamicum SMP gene can be used in vectors (II) for
 expression in host cells and production or modulation of production of
 fine chemicals, such as, an organic acid, a proteinogenic or
 nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
 nucleoside, a nucleotide, a saturated or unsaturated fatty acid,
 a diol, a carbohydrate, an aromatic compound, a cofactor, a
 polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
 encoded by them are used for diagnosing the presence or activity of
 Corynebacterium diphtheriae in a subject. (I), (III) or host cells
 containing them are used to map genomes of organisms related to C.
 glutamicum, identify and localise C. glutamicum sequences of interest, in
 evolutionary studies, in determining SMP protein regions required for
 function, in modulating SMP protein activity, in modulating the
 metabolism of sugars, and in modulating high-energy molecule production
 in a cell (i.e. ATP, NADPH)
 QY 3 Sequence 1719 BP; 405 A; 457 C; 468 G; 389 T; 0 U; 0 Other;
 QY 4 Query Match 47.2%; Score 1708; DB 4; Length 1719;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1719; Conservative 0; Mismatches 0; Indels 1; Caps 1;
 QY 5 PR 48 GAAGTCGTGCAAGGTCAAGGGAGTTGCCGAAACATGGAGGAAACAAAACCGAT 107
 Db 1 GAAGTCGTGCAAGGTCAAGGGAGTTGCCGAAACATGGAGGAAACAAAACCGAT 60
 QY 6 PR 108 GTTGTGATTGGGGAAATGGGGGTTACGATACTAGGACGGCAGTGACTGCTATCACCCTRGG 167
 Db 61 GTTGTGATTGGGGAAATGGGGGTTACGATACTAGGACGGCAGTGACTGCTATCACCCTRGG 120
 QY 7 PR 168 CGGTCTCTTGTGAAAGGAAATTACTCTAGTGTGACTCACACATCTTCAACGTTTC 227
 Db 121 CGGTCTCTTGTGAAAGGAAATTACTCTAGTGTGACTCACACATCTTCAACGTTTC 180
 QY 8 PR 228 AGCATTCAAAAGATCTGGTAGGAAACGGGGAAATGGGGTCCGTGC 287
 Db 181 AGCATTCAAAAGATCTGGTAGGAAACGGGGAAATGGGGTCCGTGC 240
 QY 9 PR 288 AGCACTCGAAACCGGTGGAGCCACGGTAGCTATTACCCCGGTGAAGATCGGGATCATT 347

RESULT 11
 ID AAF71419 standard; DNA; 1719 BP.
 DT 30-APR-2001 (first entry)
 XX Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:119.
 DE AC; XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX OS Corynebacterium glutamicum.
 XX PN WO200100844-A2.
 XX PD 04-JAN-2001.
 XX PR 23-JUN-2000; 2000WO-IB000943.
 XX PR 25-JUN-1999; 99US-0141031P.
 PR 08-JUL-1999; 99DE-01031412.
 PR 08-JUL-1999; 99DE-01031413.
 PR 08-JUL-1999; 99DE-01031419.
 PR 08-JUL-1999; 99DE-01031420.
 PR 08-JUL-1999; 99DE-01031424.
 PR 08-JUL-1999; 99DE-01031428.
 PR 08-JUL-1999; 99DE-01031431.
 PR 08-JUL-1999; 99DE-01031433.
 PR 08-JUL-1999; 99DE-01031434.
 PR 08-JUL-1999; 99DE-01031510.
 PR 08-JUL-1999; 99DE-01031562.
 PR 08-JUL-1999; 99DE-01031634.
 PR 09-JUL-1999; 99DE-01032180.

PR 27-AUG-1999; 99DE-01040765.
 PR 31-AUG-1999; 99US-0151572P.
 PR 03-SEP-1999; 99DE-01042076.
 PR 03-SEP-1999; 99DE-01042079.
 PR 03-SEP-1999; 99DE-01042086.
 PR 03-SEP-1999; 99DE-01042087.
 PR 03-SEP-1999; 99DE-01042088.
 PR 03-SEP-1999; 99DE-01042095.
 PR 03-SEP-1999; 99DE-01042123.
 PR 03-SEP-1999; 99DE-01042125.
 XX PA (BADI) BASF AG.

XX PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 XX DR WPI: 2001-061975/07.
 DR P-PSDB; AAB79303.

XX PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes.

XX PS Claim 3; Page 321-323; 1246pp; English.

XX CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).

XX SQ Sequence 1406 BP; 325 A; 381 C; 385 G; 315 T; 0 U; 0 Other;

Query Match 38.5%; Score 1395; DB 4; Length 1406;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;
 Matches 1406; Conservative 0;

QY 361 GCTTCTGAAGCTGTCGCATTGGTACCGAAGGCTCACCAAGTCAGTCAAGGTAACCTGGACATC 420
 Db 1 GCTTCTGAAGCTGTCGCATTGGTACCGAAGGCTCACCAAGTCAGTCAAGGTAACCTGGACATC 60

QY 421 GATGAATTATCGGTGAGTAAAGTTAACCGGTTAACGGTACCCGGATAACGGCATTACTTTATT 540
 Db 61 GATGAATTATCGGTGAGTAAAGTTAACCGGTTAACGGTACCCGGATAACGGCATTACTTTATT 120

QY 481 TTCCCTGTGAAATGCCAGTTCAGGTACGGTAAAGCAAGTGCCTAACGGTACCGGC 480
 Db 121 TTCCCTGTGAAATGCCAGTTCAGGTACGGTAAAGCAAGTGCCTAACGGTACCGGC 180

QY 541 GGCCCAACCCCAAGAGGTTCTTGTACCGGTGATAAGTCTCGGGTAACCGCCGG 600
 Db 181 GGCCCAACCCCAAGAGGTTCTTGTACCGGTAAACGGC 240

QY 601 AAGAAGGCTGGTCTGCCAGTTCAGGTAAAGCAAGTGCCTAACATCAAGGATCTGGCCACTGCCAACGGTAC 660
 Db 241 AAGAAGGCTGGTCTGCCAGTTCAGGTAAACATCAAGGATCTGCCAACGGTAC 300

QY 661 GTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGCCAGTTCGGCTGGTGGC 720
 Db 301 GTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGCCAGTTCGGCTGGC 360

RESULT 13	SQ	Sequence 3381 BP; 542 A; 1154 C; 1196 G; 489 T; 0 U; 0 Other;
ID	ACA37896	Standard; DNA; 3381 BP.
XX	AC	ACA37896;
XX	DT	19-JUN-2003 (first entry)
XX	DS	Prokaryotic essential gene #19553.
XX	KW	Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
XX	KW	Mycobacterium avium.
OS	XX	Mycobacterium avium.
PN	XX	WO200277183-A2.
XX	PD	03-OCT-2002.
XX	PF	21-MAR-2002; 2002WO-US009107.
XX	PR	21-MAR-2001; 2001US-00815242.
PR	06-SEP-2001; 2001US-00948993.	
PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2002; 2002US-00072851.	
PR	06-MAR-2002; 2002US-0362699P.	
XX	PA	(ELIT-) ELITRA PHARM INC.
PI	Wang L,	Zamudio C,
PI	Wall D,	Malone C,
PI	TRawick JD,	Carr GJ,
XX	DR	Haselbeck R,
XX	WPI:	Yamamoto R,
XX	DR	Forsyth RA,
XX	DR	Xu HH;
XX	PT	2003-029926/02.
PT	PT	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX	PS	Claim 14; SEQ ID NO 25766; 1766pp; English.
XX	CC	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> , <i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Qy	Sequence 3381 BP; 542 A; 1154 C; 1196 G; 489 T; 0 U; 0 Other;
ID	Qy	Query Match 37.6%; Score 1361.6%; DB 7; Length 3381;
XX	Qy	Best Local Similarity 63.2%; Pred. No. 0;
AC	Db	Mismatches 0; Conservative Matches 2131; Gaps 2;
XX	Qy	238 AAGATCTTGGTAGCAAACCGGGCGAAATCGGGTCCGTGCTGGCAGCACTCGAA 297
XX	Db	10 AAAGTCCCTGGTGCTGCCAACCGGGGGAGATCGGATCCGGCTACGGAG 69
DS	Qy	298 ACCGGTGCAGCACGGTAGCTATTACCCCCGTAAAGATGGGATCATTCACCGCTCT 357
XX	Db	70 CTGCAAATGGCACCGTGGCGGTATCCCTACGAGCACCGAATTGGTACCGGTG 129
KW	Qy	358 TTGCTTCTGAAGCTGTCCGGATTTGGTACCGAAGGTACCGGATAAC 417
KW	Db	130 AAGGCCGACGAGTGTCTACAGATGGTACCGACCGTAAACCGCC 189
XX	Qy	418 ATCGATGAAATTATCGGTGAGCTAACGGATGCCATTACCGGGATAAC 477
XX	Db	190 GTCGACGAGATGTCTACGGCTGGCTGGGCTACCTGTCTACCCGGCTAC 249
PR	Qy	478 GGCTTCTGTCTGAAATGCCAGCTGTGCCGGAAACGGCATTACTCTTT 537
PR	Db	250 GGCTTCTGTCTGGAGAACCCGATCAGGTCACCGRTC 309
PR	Qy	538 ATTGGCCAACCCAGGGTTCTTGTATCTACCGGTATAAGTCTCGGGTAACCGCC 597
PR	Db	310 GTGGCCCAAGGCCAGGGTGTGAGCTACGGGACAGTTCGGGGCATCGGGCG 369
XX	Qy	598 GCGAAGAAGGCTGTGGTAGCTGGGAAATCCACCCGAGAAAACATCGATGAG 657
XX	Db	370 GCGGGGGCGGGCTTCCGGTGTGGCTCCCTCGCCCTCGACCTCGGGTCAAGGGAG 429
XX	Qy	658 ATCGTTAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTGGCGGTGT 717
XX	Db	430 TTGGTGGAGCGAGATGACGTTCGGCTGGCTTCACCTGTATGAGCTTGC 429
XX	Qy	718 GCGGACGGGTTATGGTTGTTGCTTCACCTGTATGAGCTTGC 777
XX	Db	490 GGGGGGGGGGTCACCGATGGCGGGGTGGGGGAGGGGATGGCGGGGATGGGGG 549
XX	Qy	778 GCATCTCGTGAAGCTGAAGGGCTTTCGGGATGGCGGTATATGTCGAACGTTGTGCTGTG 837
XX	Db	550 GCGAGCGGTGAGGGGACTGAGGGTCCGGTGTGGGGACGCCCTCGGTGTTCTGAGGGGGTGTG 609
XX	Qy	838 ATTAACCCTTCAAGCATATTGAAGTGGAGATCCTGGCATCACACTGGAGAAGTTGTACAC 897
XX	Db	610 ATCAATCCGGGACATCGAGGTCCAGATCGAGGTGATGCCCG 669
XX	Qy	898 CTTATGAACTGTTGGATTCAGAAACTGCGTGTCACTGGGATGAGTTGTACAC 957
XX	Db	670 CTCACGAGGGGACTGAGGGTCCAGATCGAGGTGATGCCCG 729
XX	Qy	958 GCACAGCATTGGTGAACCAAAAGTTGTCAATTGGCAATTGGGCCA 1017
XX	Db	730 GCGCCCAACCTGGATCCGGGCTGGCTGGCAACGTGAGTTCGGTGGGGTGTGCGCA 789
XX	Qy	1018 CGCTCCATTGGTACCAAGGGGAAACCGTGGGAATTCTGGTCGATGAAAAGGGCAAC 1077
XX	Db	790 CGAGGCACTGGCTACACCTGGGGCACTGTGGTGGAGTTCTGCTGAGGAACGGGCAAC 849
XX	Qy	1078 CACGTTCTCATCGAAATGAAACCAAGTCCAGGTGACTGAAGAAAGTC 1137
XX	Db	850 CACGAGGTGGACCTGGTGAAGGGCAACCGTGGAGGACACGGTGGAGGATC 909
XX	Qy	1138 ACCGAGGTGGACCTGGTGAAGGGCAACCGTGGAGGACACGGTGGAGGAGTC 1197
XX	Db	910 ACCGAGCTGACCTGGTGGCTGGCTGGAGGAGTC 969
XX	Qy	1198 TTGGGTCTGACCCAAAGATAAGATCAAGACCCACGGTGCAGCACTGGCGCATCACC 1257

Db	970	ATGGCCTAGCCAGGATTGGTCACTCTCACGGGGCCCTGCAGTCACCCTGACCGGTACCGTCA	1029	Qy	2338 GATATGGCTGGTCTGCCAGCTGGTAACCAAGCTGGTCAACGCCACTGGCCGT 2397
Qy	1258	ACGAAGATCCAACAAACGGTTCCGGCCAGATACCGGTACCGTCA	1317	Db	2110 GACATGGCCGACTGCGGCTGGCTGGCTGGCTGGCTGAAGTCTG 2169
Db	1030	ACGGAGGACGGCCAAACGGGTTCCGGCCAGACACCGGGCATACCGCTAACGGCACC	1089	Qy	2398 GAATCGATCTGCCAGTGCACGGTCAACTGCCGGGGCCAGCTGGCAACC 2457
Qy	1318	CGAGGGGAGGTGGGTTGACGCTCACTCGGTGGAAATACCGCCA	1377	Db	2170 CGGTGACCTGGTGCACGTGCAACCCATGACAGGGGACAGCTGGGACC 2229
Db	1090	CGGGGTTGGGGCATCCGGGACGGGACCCGGCTGGAGATCAGGCG	1149	Qy	2458 TACTTGGTGCAGGTCAGCTGGTGGCAGATGCTTGCAGCGGACTACTGGTCT 2517
Qy	1378	CACTTGACTCCATGGTGGTGGCTCCGACTTGGTAACACTGGTGT	1437	Db	2230 TAGTGGGGCTGGCAGGCCGGCGATGCGGTCAGCGGGCC 2289
Db	1150	CACTTCGATTCGATGCTGACCTGGGACTCTCCCACGGGGT	1209	Qy	2518 GGCAACCCTCCAGGCCATCCCTGCTGCCATTGGTGCATTGGCTG 2577
Qy	1438	GCTCGTCAAGCGGTTGGGTGAGTTACCGGTGTCTGACCAACCATGGT	1497	Db	2290 GGAAACCAGGCAAGGGCACTATGGTGGATCTGGGCG 2349
Db	1210	GGGGGGGGGGATCCGGATTCGGGACGGGATATCCGGATATCCCG	1269	Qy	2578 GATACCGGTTGAGCCTCGAGGCTGTTCTGACCTCGAGCGGT 2637
Qy	1498	TCTTGGTGGGTTGGCTGGGGAAAGGGACTCACTTCAGGCCACGGATT	1557	Db	2350 GACACGGGTRGCCCCCTGCGGATCTGGAGGGCTGCGA 2409
Db	1270	TTCCTGCAAGGGTTCTGGACGACCCGGATTTCAGGTGGGATC	1329	Qy	2638 GGACTGTACCTGCCATTGGTGGCTGCTGGAAACCCAGGCCAACCGG 2697
Qy	1558	ATTGGCGATCACCCGGACCTCCCTCAGGCTCACCCTGCTGATGAGTC	1617	Db	2410 AAGGATAACGCTCCCTTCGAATCGGTGGCTACTGGGACTTACAC 2469
Db	1330	ATCGAACAGGGCGGAGTTGGCTCACCGGGCATCACACTCGT	1389	Qy	2698 GAAATCCCAGGGGACAGTTGTCACCCCTGCTGGGACTGCCA 2817
Qy	1618	CTGGATTACTTGGCAGATGTCACCGTGAACZAGCCTCATGGTCAAAGGATGTT	1677	Db	2470 GAGATCCGGGGCCAAATGTCGAATCTGGTCAAGGGGATCTGGG 2529
Db	1390	CICAACACTTGGCATGACAAGGTGACGTGACGGGACACCAAGATC	1449	Qy	2758 GATGTTTCACTGAAAGACAACTAAGCAGCCGTTAATGAGATGCTGGGACTGCCA 2757
Qy	1678	GCAGGTCTTATCGATAAGCTGGCTCACTGCCACCGGGTCCCGT	1737	Db	2530 GACGGGTTGAGGACATGZRAAACGGCTAGCCGGGCTAGCGCT 2589
Db	1450	TACCCGGATGACAAGGTGCCCACATGACCTGGCCACGGCCGGCTCAAG	1509	Qy	2818 ACCAAGGTCACCCCATCCTCCAAGGTTGTTGGTGGCG 2877
Qy	1738	GACCGCCCTGAAAGCCTGGCCAGCCGGGATTCGGCTGGAGGACGGA	1797	Db	2590 GTCAAGGTCAACACGTCAGGACTCTGGCTGGGCAACCTGGGATTGGGAC 2649
Db	1510	CAAGGGTTGACCGAACTTGGGGCCAGGGGATTCGGCTGGAGTGGCG	1569	Qy	2878 GGTGTTGGATCCAGGAGACTTGGTGCCTGGGACATCCAGACTCTGTC 2937
Qy	1798	CTGGCAGTTACTGATAACCACTTCCGGGATGCAACCCGGAGTC	1857	Db	2650 GGTGTTGGGGCGAGGACTCTGGCTGGGCTAGCCGGGCTAGCG 2709
Db	1570	GTGGGGTACCGAACCCAGTCCGGGACGGGACCCGGGACCCGGGT	1629	Qy	2938 ATCGCGTTCTGGCTGGGGGAGCTTGGTAACCCCTCCAGGTGGCTGGG 2997
Qy	1858	CGCTCATTCGCACTGAAAGCCTGGCTGGCCAGGGGATTCGGCTGGG	1917	Db	2710 ATCGGTTTCTGGCTGGGCTGGGACGGGCTGGGCTGGG 2769
Db	1630	CGCACCAAGGGCTGCTCAAGGGGACGGGACTTACGGGACCATCGCA	1689	Qy	2998 ACCCGGGACTGGAAAGGCCACCTCTGACGGAAAGTTCTGGAGGAA 3057
Qy	1918	CCGGTGGGAGGGCTGGCGGACCTTACGGATGGGGATGCCAAGCTGGT	1977	Db	2770 ACCAAGGCCCTAACGGGCGGAAACGGGCTGGGCAACACCTCT 2829
Db	1750	CCGGTGGGAGGGCTGACGGGCTGGGGGAGGGACTACGGGACCATCGCA	1809	Qy	3058 GAGCAGGGCACCTCGACGGCTGATGATTCCAAAGGAACCTCAACGCCCT 3117
Qy	2038	CTTCGGGGCAAACACCGGGATAACCCGGTACCCAGACTCCGCTGGCG	2037	Db	2830 GAAGGGGGTTGGCCGGGGCAACGGGCTGGGCAACGGGCTGGG 2883
Db	1810	CTGGTGGGAGGGCTAACACCGGGTACACGGGCTGGGGATGCCAACATCGCA	1869	Qy	3118 CTGGTGGATGATGTCGTAATCTCTAGGGCTGGTGAAGGGGGAGACTTTCG 2943
Qy	2098	GTTAAGGAAGCTGGCAAGCTCCGGTGGACATCTCCGACGGCTTAACGAC	2157	Db	3178 GCGGTGGATGTCGTAATCTCTAGGGCTGGTGAAGGGGGAGACTTTCG 3237
Db	1870	GTGGGGAGGGGACGGGACCGGCAATCGACGGACTCTGGTAGCCGAG	2129	Qy	3194 GGGCTGAGGCGCAACCAAGTCTCTAGGGATGGGCTGGG 3003
Qy	2158	GTCTCCAGATGGTCCAGCAATCGACGGACTCTGGTAGCCGAG	2217	Db	3238 CTGGCCAGATGCGCAATGGCTGGCTGGATGGCGATCTGAGCC 3297
Db	1930	GTGACTCGATGGCTTATCTGGTGAATCTCTGACGGCTTAACCTGGAT	1989	Qy	3004 CT---CGAGGGCTGGGCTGGAGTTGCTGATTCGGGCAATTCGGG 3157
Qy	2218	GTGGCTATGGCTTATCTGGTGAATCTCTGACGGCTCACTTGGCC 2277	Db	3061 CGGGCATGGCAACGGCTGGGCAATGGCTGGGGGGGGGG 3120	
Db	1990	GTGGGGATGGCTTACACGGGACCTGGCTGGGAGGGGGGGGGGG 2049	Qy	3358 GACCGGCTCGGTGAGTCCGACGGGAGATTCCAAACAAAGGGC 3417	
Qy	2278	TACTACCTAAAGATGGCAGGGAGATGTCAGTCTGGCTCACATCTGGCC 2337	Db	3121 GACCGCAGGCACTGGCCATGGACGGCCAGGGGGGGGGGGGGGG 3180	
Db	2050	TATTAACCTGAGCTGGCGACCAAGTGGCTGGGATCAAG 2109			

QY 3418 CATGTTGGCACCATTGGTGTGCTAACCGTGACTGTTGCTGAAGGTGATGAGGTC 3477
 Db 3181 CACATCGCTGCCCGTTCGCCGGTGGTCAACGGTCCGGCAGGTGGCAGGGTC 3240
 QY 3478 AAGGCTGGAGATGGCAATCATGAGGCTATGAAAGATGGAAACAATCACTGGCT 3537
 Db 3241 GAGGCCGGCAGACCATCGCGAAGCATGAGGCGATGAGATGGAAAGGCCGCTACCAGC 3300
 QY 3538 TCTGTTGACGGAAAATCGATCGCGTTGTCGTTCTGTGCAACGAAAGGTGGGC 3597
 Db 3301 CGGAAGTGGCAAGGTGGCGGAATGCCGTRCGGGACCGCTCAAAGTCGAGGGGGC 3360

QY 3598 GACTTGATCGTGT 3611
 Db 3361 GACCTCCGTGATGGT 3374

RESULT 14
 ACA40756
 ID ACA40756 standard; DNA; 3384 BP.
 XX
 AC ACA40756;
 XX DT 19-JUN-2003 (First entry)
 XX DE Prokaryotic essential gene #224413.
 XX KW Antisense; db; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX OS Mycobacterium tuberculosis.
 PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen RL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 DR P-PSDB; ABU36886.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 28626; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway; (8)
 CC required for proliferation, or that inhibits cellular proliferation or the biological
 CC identifying a gene required for cellular proliferation-required gene or its gene product lies
 CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX Sequence 3384 BP; 574 A; 1061 C; 1148 G; 601 T; 0 U; 0 Other;

Query Match 35.7%; Score 1294.4; DB 7; Length 3384;
 Best Local Similarity 62.0%; Pred. No. 0;
 Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;

Qy 238 AAGATCTTGGTAGCCAACCGGGAAATCGCGGTCCGTGCTTTCCGTGAGCACTCGAA 297
 Db 10 AAGTGTCTCGCCAAATCGCGGGAGATCGGAATCCGGGCTTCTGGCCCTACGAA 69

Qy 298 ACCGGTGCAGGCCACGGTAGCTATTACCCGGATACTTCCACCGCTCT 357
 Db 70 CTGGGCGTCCGGAAACCGTGGCTTATCGTACGAGGACCGCAATTGGCATACCTGTCTC 129

Qy 358 TTGCTTCTGAAGCTGTGCAATTGGTACCGAAGGGCTCACAGTCAGGGTACCTGGAC 417
 Db 130 AAGGGGACGAGTCTTACAGATGGGACATCGGATACCTGTGCAATCTGTCTCG 189

Qy 418 ATCGATGAAATTATGGTAAAGGATACTGGCATTTACCGGGATAC 477
 Db 190 GTGAGCGAGATCTGGTGCAGGGCCGTGGGGGGGTGCGACGGCCAGCTATCTACCTGGCTAC 249

Qy 478 GGCTTCCCTGTGCTGAAAATGCCAGGTTGCCAGGTTGCGAGGTGCGGAAACGGCAATTACTTTT 537
 Db 250 GGTTTTCTATGGAGATTCGGGATCTGGGATCTGGGATCTGGGATCTGGCTTC 309

Qy 538 ATTGGCCCAACCCCAGAGGTTCTGATCTCACCGGTATAAGTCTGGGGATAACCGCC 597
 Db 310 GTGGTCCCAAGGCCATGGCTGAGTGGCTGGGATAATAGTCTGGGGCATCGGGCC 369

Qy 598 GCGAAGAAGGGCTGGTGCAGGTTGGGAATCCACCCGAGGAAACATCGATGAG 657
 Db 370 GCCGGCGAAGCCGGCTTGGCTGAGTGGCTGGGATCTGGGTGACGAA 429

Qy 658 ATCGTTAAAGGGCTGAAAGCCAGACTTACCCCATCTTGTGAAAGGCAAGTGGCTGGT 717
 Db 430 CTGCTGTGGTGGGGATATGCGTGGCTGGTCAAGGGCAAGTGGCTGGGC 489

Qy 718 GGCGGAGCGGGTATGGCTCACCTGATGAGCTGGCTGGGATCGAAGGCC 777
 Db 490 GGGGGCGGGGTATGCGTGGCTGGGGATATGCGGAGGCAACCTGGGGCTGGCTGGGCC 549

Qy 778 GCATCTCGTGTGAAAGCTGAAAGGGCTTGGGGATGGCTGGTGTG 837
 Db 550 GCCAGCGGGAGCCAGTGGCTGGGACCCGACGGCTATCTGGAGGGCAGTG 609

Qy 838 ATTAACCTCAGCATATTGAGTGCAGATCTGGCATACACTGGAAAGTTGTACAC 897
 Db 610 ATCAATCCACGCCATCGAGGTGAGATTCTGGGGACAACCTGGGAGCTGGCCAT 669

Qy 898 CTTATGAACGTGACTGCTCACTGAGCTGAGTGTGCTGAAATTGGGCCA 957
 Db 670 CTCTATGAGGGTGAAGTGTGAGCTGAGGTCTGGCTGGCCCC 729

Qy 958 GCACAGCATTGGATCCAGAACTGGTGTGATGCGATTGTGGGATGAGTAAAGTCTGTC 1017

Db	730	GCGCCGACCTGGACGCCGAGTTGGTTACAAGATGTGGTGTGATGGCCTTCGCC	789	Qy	2098	GTTAAGGAAGGCTGCCAGTCCGGCTGGCATCTTCGACGCGCTTAACGGAC	2157
Qy	1018	CGCTCCATTGGTACCAAGGGGGAAACCGTGGAAATTCTTGGTCGATGAAAC	1077	Db	1870	GTGCAAGAACGGCAACGCCAACGGGAAAC	1929
Db	790	CGCCATATCGGGTACAGCTGGGGCACCGTGAGTTCTGGTGGACGGAGGGAG	849	Qy	2158	GTCTCCAGATGCGTCCAGGAATCGACCGAGTCCTGGAGACCAACCGGGTAGCGGAG	2217
Qy	1078	CAGTCTTCATCGAAATGAAACCCACGTATCCAGGTTGAGCACACCGTGAAGTC	1137	Db	1930	ATCGAGTCATGCGTCCGGGATGACGGAGTACGGGAGATTGAGAGAA	1989
Db	850	TATGTTCTCATCGAGATGAACTCCGGGGTTCAAGTGGGACACGGGAGATT	909	Qy	2218	GTGGTATGGCTTATTCTGGTGTACTCTCTGATCCAATGAAAGCTACACCCCTGGAT	2277
Qy	1138	ACCGAGGTCGACCTGGTGAAGGGGGAGATGCGCTGGTCAACCTTGAAGGA	1197	Db	1990	GTGCGGATGTGCTACACGGGACCTAACCGGAGATGGGAGTACGGTGGAC	2049
Db	910	ACCGACGTCGACCTGGGAGGACATGGCCAGGCTGGCAACTACAGTGGGATCAC	969	Qy	2278	TACTACCTAAGATGGGAGAGATCTGAAGTCTGGGTGTCACATCTGGCCATTAAAG	2337
Db	970	TGGGCTTGGGGTGGACCTGGGAGGACATGGCACCGGATGGGCAACTACAGTGGGATCAC	1029	Db	2050	TACTACCTGAAACTGGGTGAGGAGATGGGAGTACGGTGGGATGAGTGGGAGATGGGAGTCAAGTGGGATCAC	2109
Qy	1198	TGGGCTGACCCAAAGATAAGATAAGACCAAGACCGTGGGACTGGAATCACC	1257	Qy	2338	GATATGGCTGGTCTGGCTCCAGGTTGGTAAACCAAGGCTGGTCAACGGACTGGCCGTT	2397
Db	1258	ACGGAAGATCCAAACAAACGGGTTCCGCCAGATAACCGGAACTATCACCGTACCGCTCA	1317	Db	2110	GATATGGCTGCTCAAGGTTGGTCAAGGCTGGGAGTGGCTGGCAGTGGCAGT	2169
Db	1030	ACCGAGGATCCGGCCAACGGGTTCCGGGAGATCAGGGCTGGCACC	1089	Qy	2398	GAATTCGATCTGCCAGTGCACGTGCAACCCCCAGACACTGGGGTGGCOAGCTGGCAACC	2457
Qy	1318	CAAGGGGAGCTGGTGAAGTGGGACTTCAAGCTCGGTGAGTGGCAATCACC	1377	Db	2170	CGCTTGACCTGGCTGACCTGGTCAACCCACGACACACGGGTTGGCAGTGGCAGC	2229
Db	1090	GCGGGGGTGGCCGACGGGCTGGGAGGACACGGGGGGATCAGGGCTGGCACC	1089	Qy	2458	TACTTGTGCGAGCTGGCTAAGGCTGGTGAAGTGGTGGAGTGGCTGGTCT	2517
Qy	1378	CACTTTGACTCCATGGTGGTAAATGACCTGGCTGGTCCGACTTGAAGACTGCTGTT	1437	Db	2230	TATGTTGGCCGTTGGCACGCCGGCGATGCCGGGGCGCGTGGCAGC	2289
Db	1150	TACTTCGACTCCATGGTGGTCAAGCTGACCTGGCTGGTACCTCCCTACGGAGTC	1209	Qy	2518	GGCACCAACCTCCAGCCAATCCCTGTCGCTGAGGCGTACTGGCTGCGTACCGTGC	2577
Qy	1438	GCTCGTGCACAGGGCTGGCTGGTCAAGCTGGCTGGTCAAGCTGGTCTGGTCAACCAACATGGT	1497	Db	2290	GGAAACGACCAAGCCAGCCCTGTCGCTGAGCTGCTGATGGCTGGCTGAGCTGAC	2349
Db	1210	AGCCGTCGGCGGGCATCGGGAGTTCCGGATCCGGGTTATCGGAATATTCCG	1269	Qy	2578	GATACCGGTTRGAGCTGGCTGAGGCTGTTCTGACGCCATTGTCGCTGAGGCTGCG	2637
Qy	1498	TTCCTGGTGCCTGGTGGTCAACCGGACTTCACTTCAAGGCATCGCCACCGGATT	1557	Db	2350	GACACGGCCTGTCGCTGAGCTGCTGATGGCTGGCTGAGCTGGGGGGTACTGGGAGGTAC	2409
Db	1270	TTCCTGGCAAGGGTCTGGATGACCGGACTCTCCGAGGACTTCACTTCAAGGAGGATT	1409	Qy	2638	GGACTGTACCTGGCCATTGGAGTCAGTGTCCAACTGGGAGCTGGCTGGC	2697
Qy	1558	ATTGCGCATCACCGGACCTCCCTCAGGCTCCACCTGCTGATGATGAGCAGGCATC	1617	Db	2410	AAAGTGTATGGCCGGTTCGAGTGTGGTTGGCCAAACTGTCCAACTTGGGAGGAA	2469
Db	1330	ATTGATGAGGGCCGAGCTGTCACCGGGGCTCGGAGCTGGGAGCCACCAAGATC	1389	Qy	2698	GAAATCCCAGGGGAGACGGTGTCCAACTGGGAGCTGGCTGGGAGGCCAC	2757
Qy	1618	CTGGATTACTTGGCAGATGTCACCGTGAACAAAGCCCTCATGGTGTCCAAAGGATGTT	1677	Db	2470	GAGATTCCGGGGCAACTGTCCAACTTGTCCAACTTGGCTTGGGAGGAA	2529
Db	1390	CTTAACCTCTGGCCGATGTCACGTCACCGATAACCCGTATGGCTGGCTCAACGATC	1449	Qy	2758	GATCGTTGGATCCAGGAGACTTCAGGAGACTCCACCTGGGAGCTGGTGGTGG	2817
Qy	1678	GCAGGCTTGAAGGAGCTGGCCAGCTGGCTGGTGGTGGTGGTGGTGGTGGTGG	1737	Db	2530	GATCGATTGGCAAGAGATGGGAGCTGGCTGGGAGCTGGCTGGGAGGCTGG	2589
Db	1450	TACCCGGACGACAAGCTGGCCGATCTGGTGTGACCGGGGCTCGGCAACCGGGGACCAAGATC	1509	Qy	2818	ACCAAGGTCAACCCCATCCTCCAGGAGACTTCAGGAGACTCCAGACTGGTGG	2877
Qy	1738	GAAGGGCTGAAGGAGCTGGCCAGCCGGGTTGGCTGGTGAATCTCCGGTGGAGCGCA	1797	Db	2590	GTGAGGTCAAGCTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGG	2649
Db	1510	CAGCGACTAGTCACGGTACCGATAACCCGTATGGCTGGCTGGGAGTGGCTGGGAGT	1569	Qy	2878	GTGTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGG	2937
Qy	1798	CTGGCAGTACTGATAACCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCT	1857	Db	2650	GGTGTCAGTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGG	2709
Db	1570	GTGGGGTACCGATAACCCGATACCGATCCGGGATGGCTACCGTGGCTACCCGAGTA	1629	Qy	2938	ATCGCGTTCCTGGCTGGGAGCTGGCTGGGAGCTGGCTGGGAGCTGG	2997
Qy	1858	CGCTCATTCGCACTGAAGCCTGGCTGGGAGGGCGAGGGCGCTGGTGGAAAGCTG	1917	Db	2710	CTCGGATTTCGG	2769
Db	1630	CGCACCAAGGGACCTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1689	Qy	2998	ACCCGGGACCTGGAAAGGCCGCTCCGAAGGCAACGGCACCTCTGACGGAA	3057
Qy	1918	TCCGTGGAGGGCTGGTGCACGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1977	Db	2770	ACTGGGGGCTGG	3117
Db	1690	TCCGTGGAGGGCAACACCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1809	Qy	3058	GAGCAGGGGACACCTGGAAAGGAGTCTGGCTGGGGGGGGGGGGGGGGGGGG	3143
Qy	1978	CCGTGGAGGGCTGG	2037	Db	2827	GACGAGATTGGCCCTATGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2883
Db	1750	CCCTGGGAACGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1869	Qy	3118	CTGGTCCCGAAGGCCAACCCGGTACCGTGGGGGGGGGGGGGGGGGGGGGG	3177
Qy	2038	CTTCGCCCCGAAACACCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2097	Db	2884	TATTTCCAGTCCAAACAAAGGAATTCAATGGGACGGGGGGGGGGGGGGGG	2943
Db	1810	TTGG	1869				

3178	GGCCTGGATCGAATTCTTACGGCCTGTCGAAGGCCCTGCTGGACTTTGATCCGC QY	3237
2944	CAATTGTCGGCCAACCAGTCTTCTATGGTCTGGCAAGGTGAAGGATCGGGTGAAG Qb	3003
3238	CTGCCAGATGTCGCCACCCCACTGCTTGCCTGGATGGCATCTGAGCCAGACGAT QY	3297
3004	CTG---GAGGGTGGGGTGGAGCTGGTGAATGGCTGGAGGCCATTTCGAACCGAA Qb	3060
3298	AAGGGTATGCCAACCGTCAACGCCAGATCCGCCAATGCGTGTGGCT QY	3357
3061	CGCGGCATGCCAACGGCATGTGCATCTCAACGGCAGCTGGCGTAGTGGCC Qb	3120
3358	GACCGCTCCGTGAGTCGTACCGCAACCGCACAAAGGCAGATTCCCAAACAAGGGC QY	3417
3121	GACCGCAGGATGCCAGTGCCTGGCCATTGGAGGCCAACCGGAAAGGGCA Qb	3180
3418	CATGTTGCTGCCACATTGCTGGTGTCAACCGTGACTTGTGAAGGTGATGAGGTC QY	3477
3181	CACATGCCGCCATTGCGGAGTCGTACGGTGGCTGCGTCGGGGTGTGGCGAGGG Qb	3240
3478	AAGGCTGGAGATGGCAGTCGCAATCATCGAGGCTATGAAAGATGGAAGCAACA QY	3537
3241	GGGGCGGCCAAACCATCGCCACCATCGGGCATGAAAGATGGAAGGCCGAT Qb	3300
3538	TCTGTTGACGGCAAATCGATCGCGTTGCTTCCTGGTGCACCGAAGGTGG QY	3597
3301	CCGGTTGCCGGCACCGTGGAGCGGGTGTGGACACCGGCCAGGGGG Qb	3360
3598	GACTTGATCGTCGTTCCCTAA QY	3621
3361	GACCTGTRGGTGGTGAAGTGA Qb	3384

RESULT 15
Aai99682_33/c
Continuation (34 of 45) of Aai99682 from base 3300001 (Mycobacterium tuberculosis strain
MP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682

WP	AAI99682_35	35000001	36100000
WP	AAI99682_36	36000001	37100000
WP	AAI99682_37	37000001	38100000
WP	AAI99682_38	38000001	39100000
WP	AAI99682_39	39000001	40100000
WP	AAI99682_40	40000001	41100000
WP	AAI99682_41	41000001	42100000
WP	AAI99682_42	42000001	43100000
WP	AAI99682_43	43000001	44100000
WP	AAI99682_44	44000001	4411529
Qy	Query Match	35.7%	Score 1294.4 ; DB 4 ; Length 110000 ;
Best Local Similarity	62.0%	Pred. No. 0 ;	
Matches 2099 ; Conservative	0 ;	Mismatches 1276 ; Indels 9 ; Gap	
Db	23034 AAGGTGCTCGCCAATCCGGGAGATCCGCGATTCGGCTTACGGCTACCGCT	238 AAGATCTTGGTAGCAAACCGCGGGAAATCCGGGGTCCGTGCAGCACTCC	
Qy	298 ACCGGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCCACCGCT	298 ACCGGTGCAGCCACGGTAGCTATTACCCCCGTGAAGAGATCGGGATCATTCCACCGCT	
Db	22974 CTGGCGCTCGGAACCCGTGGCCGTTATCCGTACGGAGACCGAACATTCCGAGCACCGCT	22974 CTGGCGCTCGGAACCCGTGGCCGTTATCCGTACGGAGACCGAACATTCCGAGCACCGCT	
Qy	358 TTTCGTTCTGAAGGCTGTCCCACATTGGTACCCAGGCTCACAGTCAGGTAAGGGTACCTGG	358 TTTCGTTCTGAAGGCTGTCCCACATTGGTACCCAGGCTCACAGTCAGGTAAGGGTACCTGG	
Db	22914 AAGGGGACGGAGTCCTTACCAAGATCGGCACATCGGTCAACGGGTGATGCCATACTGGCT	22914 AAGGGGACGGAGTCCTTACCAAGATCGGCACATCGGTCAACGGGTGATGCCATACTGGCT	
Qy	418 ATCGATGAAATTATCGGTGAGCTAAAGGTTAAAGCAGATGCCATTACCCGGATCTACCTGGCT	418 ATCGATGAAATTATCGGTGAGCTAAAGGTTAAAGCAGATGCCATTACCCGGATCTACCTGGCT	
Db	22854 GTCGACGAGATCGTCGGGACGGCCCGTGGCGACGGCCGATGGCGACGCTATCTACCTGGCT	22854 GTCGACGAGATCGTCGGGACGGCCCGTGGCGACGGCCGATGGCGACGCTATCTACCTGGCT	
Qy	478 GGCTTCCCTGTCGAAAATGCCAGCTTGGCCAGGTGTGGGAAACCGGCATTACT	478 GGCTTCCCTGTCGAAAATGCCAGCTTGGCCAGGTGTGGGAAACCGGCATTACT	
Db	22794 GGGTTTCTATCGGAGAATCCGGATCTGGCTGGCATCGGGGGATCAGCC	22794 GGGTTTCTATCGGAGAATCCGGATCTGGCTGGCATCGGGGGATCAGCC	
Qy	538 ATTGGCCAACCCAGAGGGTCTGTATCTCACCGGTGATAAGTCTCGCGGTAACC	538 ATTGGCCAACCCAGAGGGTCTGTATCTCACCGGTGATAAGTCTCGCGGTAACC	
Db	22734 GTCGGTCCAGGGCGAAGGTGGCTGAGCTGGCTGGAAATAAGTCTCGGCCATCGGG	22734 GTCGGTCCAGGGCGAAGGTGGCTGAGCTGGCTGGCTGGAAATAAGTCTCGGCCATCGGG	
Qy	598 GCGAAGAAGGCTTGGCTGCCAGACTTACCCATCTTGTGAAGGCAGTTGGCGGT	598 GCGAAGAAGGCTTGGCTGCCAGACTTACCCATCTTGTGAAGGCAGTTGGCGGT	
Db	22674 GCCCGGAAGCCGGCTTGCCCGGATGCCGTTCCGRTGTCGTCAAGGCAGTTGGCGGT	22674 GCCCGGAAGCCGGCTTGCCCGGATGCCGTTCCGRTGTCGTCAAGGCAGTTGGCGGT	
Qy	658 ATCGTTAAAGGGCTGTAAGGCCAGACTTACCCATCTTGTGAAGGCAGTTGGCGGT	658 ATCGTTAAAGGGCTGTAAGGCCAGACTTACCCATCTTGTGAAGGCAGTTGGCGGT	
Db	22614 CTGCTGTGGTGGCCGGATGCCGTTCCGRTGTCGTCAAGGCAGTTGGCGGT	22614 CTGCTGTGGTGGCCGGATGCCGTTCCGRTGTCGTCAAGGCAGTTGGCGGT	
Qy	718 GGGGGCCGGGTATGCCATCGGTGTCGGGATATCGGAAATTAGCAACAA	718 GGGGGCCGGGTATGCCATCGGTGTCGGGATATCGGAAATTAGCAACAA	
Db	22554 GGGGGCCGGGTATGCCATCGGTGTCGGGATATCGGAAATTAGCAACAA	22554 GGGGGCCGGGTATGCCATCGGTGTCGGGATATCGGAAATTAGCAACAA	
Qy	778 GCATCTCGTGAAGGCTGAAGGGCTTTCGGCGATGGGGTATATGTCGAACTGGCT	778 GCATCTCGTGAAGGCTGAAGGGCTTTCGGCGATGGGGTATATGTCGAACTGGCT	
Db	22494 GCCAGCCGGGAAGCCGAGTCGGCTGGGACCCAGGGTCTATCGGAGGCC	22494 GCCAGCCGGGAAGCCGAGTCGGCTGGGACCCAGGGTCTATCGGAGGCC	
Qy	838 ATTAACCCTCAGCATATTGAAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTA	838 ATTAACCCTCAGCATATTGAAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGTA	
Db	22434 ATCAATCCACGCCACATCGAGGGTGCAGATTCTGGGGGACAACTCGGAGCTGATCGAA	22434 ATCAATCCACGCCACATCGAGGGTGCAGATTCTGGGGGACAACTCGGAGCTGATCGAA	
Qy	898 CTTTATGAAACGTGACTGCTCACTGCAGCGTCTGGTCAACCAAAAGTTGCGA	898 CTTTATGAAACGTGACTGCTCACTGCAGCGTCTGGTCAACCAAAAGTTGCGA	
Db	22374 CTCATGACGGTGAATGGCTTACAAGATGTCGGTCCATCGAGGTCAATCGGAGCTGGCT	22374 CTCATGACGGTGAATGGCTTACAAGATGTCGGTCCATCGAGGTCAATCGGAGCTGGCT	
Qy	958 GCACAGGATTGGATCCAGAAACTGCTCACTGCAGCGTCTGGTCAACCAAAAGTTGCGA	958 GCACAGGATTGGATCCAGAAACTGCTCACTGCAGCGTCTGGTCAACCAAAAGTTGCGA	
Db	22314 CGCCGCACCTGGACGGTACAGCTGGGACGGTACAGCTGGGACGGTACAGCTGGGACGG	22314 CGCCGCACCTGGACGGTACAGCTGGGACGGTACAGCTGGGACGGTACAGCTGGGACGG	
Qy	1018 CGCTCCATTGGTACCGGGCGGGAAACCGTGGAAATTCTGGTGCATGGCTTCCGCT	1018 CGCTCCATTGGTACCGGGCGGGAAACCGTGGAAATTCTGGTGCATGGCTTCCGCT	
Db	22254 CGCCCATATCGGTAACAGCTGGGACGGTACAGCTGGGACGGTACAGCTGGGACGG	22254 CGCCCATATCGGTAACAGCTGGGACGGTACAGCTGGGACGGTACAGCTGGGACGG	
Qy	1078 CACGTTCTTICATCGAAATGAAACCCAGTATCCAGGTGAGGCACACCGTAAAGGAA	1078 CACGTTCTTICATCGAAATGAAACCCAGTATCCAGGTGAGGCACACCGTAAAGGAA	

3298	AGGGTATGCCAATGTTGTGGCCAACGTCAACGCCAGATCCGCCAATGCGCTGTGGT Y	3357
19983	CGGGCATGCCAACGGTATGTGCATCCTCAACGGCAGCTGGCGGTAGTGC b	19924
3358	GACCGCTCCGTTGAGTCACCGCAACCGCAAGAAAGGCCAGATCCTCAACAGGGC Y	3417
19923	GACGGCAGCATGCCAGTGGCTCCGGTGGCTGACTGTTGCTCACCGTGAAGGTGATGAGG b	19864
3418	CATGTTGCTGCACCATTGGCTGGTGTGACTGTTGCTGAAGGTGATGAGG Y	3477
19863	CACATGCCGCCATTGGGAGTCGTCAAGGTGGCTGGGGTGGCTGGGAGGGTC b	19804
3478	AAGGCTGGAGATGGCAGTCGCAATCATCGAGGCTATGAAAGATGGAAGGCAACA Y	3537
19803	GCGCCGCCAACCATCGGCCACCATCGAGGCATGAAAGATGGAAGGCCGATC b	19744
3538	TCTGTTGACGGCAAAATCGATCGCGTTCTGCTGCAACGAAGGTGGAAAGG Y	3597
19743	CGGTTGCCGGCACCGTGAGGGTGGGGTGTGGACACCCGCCAGGTGGAGGG b	19684
3598	GACTTGTATCGTCGTTCTGCTTA Y	3621
19682	CGCTCTTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG b	19660

Search completed: March 23, 2004, 18:35:43
Job time: 1318 secs

Copyright (c) 1993 - 2004 Compugen Ltd.

DOM nucleic - nucleic search, using sw model
Run on: March 23, 2004, 17:20:33 ; Search time 237 Seconds
(without alignments)
252025 matches found in 1000000 / 1000000

Title: US-10-045-072-1
Perfect score: 3621
Sequence: 1 tggggggggtagatccctg.....tggatcgatcgtttcctaa 3621

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

```
Database : Issued_Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*
```

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	100.0	3621	3	US-09-220-081-1
2	3621	100.0	3621	4	US-09-677-575-1
3	1294.4	35.7	4403765	3	US-09-103-840A-2
C	1294.4	35.7	4411529	3	Sequence 1, Appli
C	1249.6	34.5	32155	4	Sequence 2, Appli
C	509.2	14.1	3492	4	Sequence 1, Appli
7	486.2	13.4	3465	4	Sequence 1, Appli
8	479.8	13.3	5030	4	Sequence 2, Appli
C	476.2	13.2	2922	4	Sequence 1, Appli
10	313.4	8.7	1362	4	Sequence 2, Appli
11	313	8.6	1362	1	Sequence 3, Appli
12	313	8.6	1362	1	Sequence 4, Appli
13	313	8.6	1362	1	Sequence 5, Appli
14	313	8.6	1362	2	Sequence 6, Appli
15	313	8.6	1362	4	Sequence 7, Appli
16	311.4	8.6	1362	1	Sequence 8, Appli
17	311.4	8.6	1362	2	Sequence 9, Appli
18	311.4	8.6	1362	3	Sequence 10, Appli
19	299	8.3	3077	1	Sequence 11, Appli
20	299	8.3	3077	5	Sequence 12, Appli
21	298.6	8.2	3065	1	Sequence 13, Appli
22	298.6	8.2	3065	1	Sequence 14, Appli
23	298.6	8.2	3065	1	Sequence 15, Appli
24	298.6	8.2	3065	1	Sequence 16, Appli
25	298.6	8.2	3065	2	Sequence 17, Appli
26	298.6	8.2	3065	2	Sequence 18, Appli
					Sequence 19, Appli

28	298.6	4	US-09-433-043B-1	Sequence 1, Appli
29	297.4	4	US-09-252-991A-2354	Sequence 2354, Ap
30	288.6	8.0	US-09-634-238-58	Sequence 58, Appli
31	284.8	7.9	US-09-328-352-3436	Sequence 3436, Ap
32	270.6	7.5	US-08-662-344-1	Sequence 1, Appli
33	263.8	7.3	US-09-252-991A-2481	Sequence 2481, Ap
34	255.4	7.1	1664976 4 US-08-916-421B-1	Sequence 1, Appli
35	251.6	6.9	1356 4 US-09-540-236-1127	Sequence 1127, Ap
36	251.6	6.9	23673 4 US-09-773-816-1	Sequence 1, Appli
37	251.6	6.9	119211 4 US-09-596-002-40	Sequence 40, Appli
38	250.2	6.9	4403765 3 US-09-103-840A-2	Sequence 2, Appli
39	250.2	6.9	4411529 3 US-09-103-840A-1	Sequence 1, Appli
40	249	6.9	2031 4 US-09-252-991A-9572	Sequence 9572, Ap
41	249	6.9	3006 4 US-09-252-991A-9720	Sequence 9720, Ap
42	247.4	6.8	19702 4 US-08-961-527-7	Sequence 7, Appli
43	247	6.8	1398 4 US-09-252-991A-10409	Sequence 10409, A
44	247	6.8	1446 4 US-09-252-991A-10752	Sequence 10752, A
45	246.8	6.8	1830121 4 US-09-557-884-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-220-081-1
; Sequence 1, Application US/09220081
; Patent No. 6171833
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/220, 081
; CURRENT FILING DATE: 1998-12-23

1 SOFTWARE: Patentin Ver. 2.0
1 SEQ ID NO 1
1 LENGTH: 3621
1 TYPE: DNA
1 ORGANISM: *Corynebacterium glutamicum*
1 FEATURE:
1 NAME/KEY: CDS
1 LOCATION: (199) . . . (3621)
1 US-09-2220-081-1

Db	301	GTTGCAGCCACGGTAGCTATTACCCCCGTGAAAGATCGGGATCATTCACCGCTCTTT	360	QY	1441	CGRGCA CAGGCCGGTGGCTGAGTTAACCGGTACCGTCAACGGACATC	1500
Qy	361	GCTTCTGAAGCTGTCCGATTGGTACCGAAGGTCAACCAACTGCTGGACATC	420	Db	1441	CGRGCA CAGGCCGGTGGCTGAGTTAACCGGTACCGTCAACGGACATC	1500
Db	361	GCTTCTGAAGCTGTCCGATTGGTACCGAAGGTCAACCAACTGCTGGACATC	420	Qy	1501	TTCGGTGCCTTGCTGGGAAAGGACTTCACTTCAAGGGATTCATT	1560
Qy	421	GATGAATTATCGGTCAAGTAAAAGTTAAGGAGATGCCATTACCCGGATAAGGC	480	Db	1501	TTCGGTGCCTTGCTGGGAAAGGACTTCACTTCAAGGGATTCATT	1560
Db	421	GATGAATTATCGGTCAAGTAAAAGTTAAGGAGATGCCATTACCCGGATAAGGC	480	Qy	1561	GCCGATCACCCGGACCTCCACCGTCAAGGTGCTGATGATGAGCCTG	1620
Qy	481	TTCCTGTCTGAAATGCCCAAGTGTGCCGAAACGGCATTACTTTTATT	540	Db	1561	GCCGATCACCCGGACCTCCACCGTCAAGGTGCTGATGATGAGCCTG	1620
Db	481	TTCCTGTCTGAAATGCCCAAGTGTGCCGAAACGGCATTACTTTTATT	540	Qy	1621	GATTACTTGGCAGATGTCACCGTCAAGGCTCATGGATGTTGCA	1680
Qy	541	GGCCCCAACCCCAGAGGTTCTGTGATAAGTCTGCGGGTAACGCCGCG	600	Db	1621	GATTACTTGGCAGATGTCACCGTCAAGGCTCATGGATGTTGCA	1680
Db	541	GGCCCCAACCCCAGAGGTTCTGTGATAAGTCTGCGGGTAACGCCGCG	600	Qy	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATCTGCTAACATCAAGGATC	1740
Qy	601	AAGAAGGGCTGGGAAATTCCACCCGAGCAAACATCGATGAGATC	660	Db	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATCTGCTAACATCAAGGATC	1740
Db	601	AAGAAGGGCTGGGAAATTCCACCCGAGCAAACATCGATGAGATC	660	Qy	1741	CGCGTGAAGGAGCTTGGCCAGACCGCTGCTGAGCCGAGTCCGC	1800
Qy	661	GTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGAGGTGGC	720	Db	1741	CGCGTGAAGGAGCTTGGCCAGACCGCTGCTGAGCCGAGTCCGC	1800
Db	661	GTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGAGGTGGC	720	Qy	1801	GCAGTTACTGATAACCACCTTCCGGATGCAACCCAGCTTGGCAGACCG	1860
Qy	721	GGACCGGGTATGGCTTCACTCTGATGAGCTTCGCAATTAGCAAGAGCA	780	Db	1801	GCAGTTACTGATAACCACCTTCCGGATGCAACCCAGCTTGGCAGACCG	1860
Db	721	GGACCGGGTATGGCTTCACTCTGATGAGCTTCGCAATTAGCAAGAGCA	780	Qy	1861	TCAATTGGCACTGAAGCCTGGGGAGACCTAAGTGGCTGAGCTTTGTC	1920
Qy	781	TCTCGTGAAGCTGCTGGGATGGGGTATATGTCGAACGTGCTGATT	840	Db	1861	TCAATTGGCACTGAAGCCTGGGGATGGGGTATGGCTGAGCTTTGTC	1920
Db	781	TCTCGTGAAGCTGCTGGGATGGGGTATGGCTGAGCTTCGCAATTAGCAAGAGCA	840	Qy	1921	GTGAGGGCTGGGGGACCTAGTGGGATAACACCCGTACCCAGACTCCG	1980
Db	841	AACCCTAGCAATTGAAAGTGCAGATCCTGGGATCAACTGGAAAGTTGACACCTT	900	Db	1921	GTGAGGGCTGGGGATAACACCCGTACCCAGACTCCGTTGGGATGTC	1980
Qy	901	TATGAACGTGACTGCTCACTGCAAGCGCTGTCACAAAGTTGCGCAGCA	960	Qy	1981	TGGCAAGGGCTGGGGGACCTAGTGGGATAACACCCGTACCCAGACT	2040
Db	901	TATGAACGTGACTGCTCACTGCAAGCGCTGTCACAAAGTTGCGCAGCA	960	Db	1981	TGGCAAGGGCTGGGGATAACACCCGTACCCAGACTCCGTTGGGATGTC	2040
Qy	961	CAGCATTGGATCCAGAACACTGGGATGGGGTACCCAGTAAAGTTGCCG	1020	Qy	2041	CGCGGGCGAACACCGTGGGATAACACCCGTACCCAGACTCCGTTGGG	2100
Db	961	CAGCATTGGATCCAGAACACTGGGATGGGGTACCCAGTAAAGTTGCCG	1020	Db	2041	CGCGGGCGAACACCGTGGGATAACACCCGTACCCAGACTCCGTTGGG	2100
Qy	1021	TCCATTGGTTACCAAGGGGGAAACCGTGGGAATTCTGGTCAACCTGAA	1080	Qy	2101	AAGGAAGGTGCACTGGGGGATGGGACATCCTTCGCACTTGGGATGTC	2160
Db	1021	TCCATTGGTTACCAAGGGGGAAACCGTGGGAATTCTGGTCAACCTGAA	1080	Db	2101	AAGGAAGGTGCACTGGGGGATGGGACATCCTTCGCACTTGGGATGTC	2160
Qy	1081	GTCTTCATCGAAATGAACTGGGGAAACCGTGGGAATTCTGGTCAACCTGAA	1140	Qy	2161	TCCCAAGATGGCTCCAGGAATCGACGGAGCTGGGGGATGGGATGTC	2220
Db	1081	GTCTTCATCGAAATGAACTGGGGAAACCGTGGGAATTCTGGTCAACCTGAA	1140	Db	2161	TCCCAAGATGGCTCCAGGAATCGACGGAGCTGGGGGATGGGATGTC	2220
Qy	1141	GAGGTGGACCTGGTGAAGGGGGAGATGGCTGGTGGCAACCTTGAGGAATTG	1200	Qy	2221	GCTATGGCTTATTCTGGTGAATCTCTGATCCAATGAAAGCTCTG	2280
Db	1141	GAGGTGGACCTGGTGAAGGGGGAGATGGCTGGTGGCAACCTTGAGGAATTG	1200	Db	2221	GCTATGGCTTATTCTGGTGAATCCAATGAAAGCTCTG	2280
Qy	1201	GGTCTGACCCAAAGATAAGATCAAGACCCACGGTCACTGCAAGTGGGCA	1260	Qy	2281	TACCTAAAGATGGAGGAGATCTGGTCAAGTGGCTGAGGATCTGGG	2340
Db	1201	GGTCTGACCCAAAGATAAGATCAAGACCCACGGTCACTGCAAGTGGGCA	1260	Db	2281	TACCTAAAGATGGAGGAGATCTGGTCAAGTGGCTGAGGATCTGGG	2340
Qy	1261	GAAGATCCAAACAAACGGCTTCGGTCACTGCAAGTGGGAAACTATCACCG	1320	Qy	2341	ATGGCTGGTCTGGCTTCGCCCCAGCTGGTCAAGTGGCTGAGGATCTGG	2460
Db	1261	GAAGATCCAAACAAACGGCTTCGGTCACTGCAAGTGGGAAACTATCACCG	1320	Db	2341	ATGGCTGGTCTGGCTTCGCCCCAGCTGGTCAAGTGGCTGAGGATCTGG	2460
Qy	1321	GGGGAGCTGGCTGGTCACTGCTGGTCACTGCAAGTGGGAAACTATCACCG	1380	Qy	2461	TTTGGCTGCAAGCTGGTCAAGTGGCTGTTGCACTGCTGGCTGGC	2520
Db	1321	GGGGAGCTGGCTGGTCACTGCTGGTCACTGCAAGTGGGAAACTATCACCG	1380	Db	2461	TTTGGCTGCAAGCTGGTCAAGTGGCTGTTGCACTGCTGGCTGGC	2520
Qy	1381	TTTGACTCCATGCTGGTAAAGTACCTGCTGGTCACTGCTGGTCACTG	1440	Db	2461	TTTGGCTGCAAGCTGGTCAAGTGGCTGTTGCACTGCTGGCTGGC	2520

2521	ACACACCTCCAGCCATCCCTCGAGGCTCGAGGCTGTTCTGACCTCGAGGCTGTTCTGCCATTGTCGCTGCTGCACTGGGAAACCCGTGCGAT	2580	Db	3601	TTGATCGTCGTTCTCTAA	3621
2581	ACCGGTTTGCCTTGAGCTTGAGTCTGGAACCCAGGCCAACCGGCTGACTTACCGCCACGGGACTGGCTTACCGCCACGGGAA	2640	Qy	2581	ACCGGTTTGCCTTGAGCTTGAGTCTGGAACCCAGGCCAACCGGCTGACTTACCGCCACGGGAA	2640
Db	CTGTACCTGCCATTGAGTCTGGCACAGGCCAACCGGCTGACTTACCGCCACGGGAA	2700	Qy	2641	CTGTACCTGCCATTGAGTCTGGCACAGGCCAACCGGCTGACTTACCGCCACGGGAA	2700
Db	ATCCCAGGGCACAGTGTCAACCTGGGACTGGGAAACCCAGGCCAACCGGCTGACTTACCGCCACGGGAA	2760	Qy	2701	ATCCCAGGGCACAGTGTCAACCTGGGACTGGGAAACCCAGGCCAACCGGCTGACTTACCGCCACGGGAA	2760
Db	CGTTTCGAACTCATCGAACAGACTACCCAGGGTAAATGAGATGCTGGGACGCCAAC	2820	Qy	2761	CGTTTCGAACTCATCGAACAGACTACCCAGGGTAAATGAGATGCTGGGACGCCAAC	2820
Db	AAGGTCAACCCATCCTCCAAAGGCTGCTGGGACCTCGCACTCCACCTCGTTGGGGGT	2880	Qy	2821	AAGGTCAACCCATCCTCCAAAGGCTGCTGGGACCTCGCACTCCACCTCGTTGGGGGT	2880
Db	AAGGTCAACCCATCCTCCAAAGGCTGCTGGGACCTCGCACTCCACCTCGTTGGGGGT	2880	Qy	2881	AAGGTCAACCCATCCTCCAAAGGCTGCTGGGACCTCGCACTCCACCTCGTTGGGGGT	2880
Db	GGGTTCCTGGCGGGAGCTTGGTAACCCAAAGTACGACATCCCAAGACTCTGTCACTC	2940	Qy	2941	GGGTTCCTGGCGGGAGCTTGGTAACCCAAAGTACGACATCCCAAGACTCTGTCACTC	2940
Db	GGGTTCCTGGCGGGAGCTTGGTAACCCAAAGTACGACATCCCAAGACTCTGTCACTC	2940	Qy	2941	GGGTTCCTGGCGGGAGCTTGGTAACCCAAAGTACGACATCCCAAGACTCTGTCACTC	2940
Db	CGCGCACTGGAAAGGCCCTCCGAAGGGCACCTCTGACGGAAGTTCCCTGAGGAAGAG	3060	Qy	3001	CGCGCACTGGAAAGGCCCTCCGAAGGGCACCTCTGACGGAAGTTCCCTGAGGAAGAG	3060
Db	CGCGCACTGGAAAGGCCCTCCGAAGGGCACCTCTGACGGAAGTTCCCTGAGGAAGAG	3060	Qy	3001	CGCGCACTGGAAAGGCCCTCCGAAGGGCACCTCTGACGGAAGTTCCCTGAGGAAGAG	3060
Db	CAGGGCAACCTCGACCGCTGATGATTCCAAGGAACCGTCAACCCCTCTGCTG	3120	Qy	3061	CAGGGCAACCTCGACCGCTGATGATTCCAAGGAACCGTCAACCCCTCTGCTG	3120
Db	CAGGGCAACCTCGACCGCTGATGATTCCAAGGAACCGTCAACCCCTCTGCTG	3120	Qy	3061	CAGGGCAACCTCGACCGCTGATGATTCCAAGGAACCGTCAACCCCTCTGCTG	3120
Db	TTCCCCGAAGGCCAACCGAACCCGAAGGAGTTCCCTACCGGCTCTGGCTGAGACT	3180	Qy	3121	TTCCCCGAAGGCCAACCGAACCCGAAGGAGTTCCCTACCGGCTCTGGCTGAGACT	3180
Db	TTCCCCGAAGGCCAACCGAACCCGAAGGAGTTCCCTACCGGCTCTGGCTGAGACT	3180	Qy	3121	TTCCCCGAAGGCCAACCGAACCCGAAGGAGTTCCCTACCGGCTCTGGCTGAGACT	3180
Db	CTGGATGATCGTGAATTCTCTACCGGCTCTGGCTGAGACTTGTGATCCGCCCTG	3240	Qy	3181	CTGGATGATCGTGAATTCTCTACCGGCTCTGGCTGAGACTTGTGATCCGCCCTG	3240
Db	CTGGATGATCGTGAATTCTCTACCGGCTCTGGCTGAGACTTGTGATCCGCCCTG	3240	Qy	3181	CTGGATGATCGTGAATTCTCTACCGGCTCTGGCTGAGACTTGTGATCCGCCCTG	3240
Db	CCAGATGTGGCACCCACTGCTTGTGAATTCTCTACCGGCTCTGGCTGAGACTTGT	3300	Qy	3241	CCAGATGTGGCACCCACTGCTTGTGAATTCTCTACCGGCTCTGGCTGAGACTTGT	3300
Db	CCAGATGTGGCACCCACTGCTTGTGAATTCTCTACCGGCTCTGGCTGAGACTTGT	3300	Qy	3241	CCAGATGTGGCACCCACTGCTTGTGAATTCTCTACCGGCTCTGGCTGAGACTTGT	3300
Db	GCTATGGCAATGTGTGGCCAACGTCACGGCCAGATCGGTGCTGCTG	3360	Qy	3301	GCTATGGCAATGTGTGGCCAACGTCACGGCCAGATCGGTGCTGCTG	3360
Db	GCTATGGCAATGTGTGGCCAACGTCACGGCCAGATCGGTGCTGCTG	3360	Qy	3301	GCTATGGCAATGTGTGGCCAACGTCACGGCCAGATCGGTGCTGCTG	3360
Db	CGCTCCGTGAGTCGCTGCACTGGCAACCGCAGAAAAGGCAGATTCTCCAAACAGGCCAT	3420	Qy	3361	CGCTCCGTGAGTCGCTGCACTGGCAACCGCAGAAAAGGCAGATTCTCCAAACAGGCCAT	3420
Db	CGCTCCGTGAGTCGCTGCACTGGCAACCGCAGAAAAGGCAGATTCTCCAAACAGGCCAT	3420	Qy	3361	CGCTCCGTGAGTCGCTGCACTGGCAACCGCAGAAAAGGCAGATTCTCCAAACAGGCCAT	3420
Db	GTTGCTGCAACCATTGGCTGGTGTGACTGTTGTGAGGTGATGAGGTCAAG	3480	Qy	3421	GTTGCTGCAACCATTGGCTGGTGTGACTGTTGTGAGGTGATGAGGTCAAG	3480
Db	GTTGCTGCAACCATTGGCTGGTGTGACTGTTGTGAGGTGATGAGGTCAAG	3480	Qy	3421	GTTGCTGCAACCATTGGCTGGTGTGACTGTTGTGAGGTGATGAGGTCAAG	3480
Db	GCTGGAGATGCACTGGCTATGAGGATGGAAAGCAACAAATCACTGCTTCT	3540	Qy	3481	GCTGGAGATGCACTGGCTATGAGGATGGAAAGCAACAAATCACTGCTTCT	3540
Db	GTTGACGGCAAATTCGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3600	Qy	3541	GTTGACGGCAAATTCGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3600
Db	GTTGACGGCAAATTCGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3600	Qy	3541	GTTGACGGCAAATTCGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3600
Db	GGCCCAAACCCAGGGTCTCTGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3621	Qy	3601	GGCCCAAACCCAGGGTCTCTGATCGCTGTTCTGCTGCAACGAAGGTGGGAC	3621

|||||
Db 2761 CGTTTCGAACTCATCGAAGACAAC TACGGAGCCGTTAATGAGATGGTGGACGCCAACC 2820
Qy 2821 AAGGTCAACCCATCCCAAGGTGTTGGGACCTCGCACTCCACACTCGTGGACTCTGGGGT 2880
Db 2821 AAGGTCAACCCATCCCAAGGTGTTGGGACCTCGCACTCGTGGACTCTGGGGT 2880
Qy 2881 GTGGATCCAGAGACTTTGCTGCCGATCCAAAAGTAGCACATCCAGACTCTGTCACTC 2940
Db 2881 GTGGATCCAGAGACTTTGCTGCCGATCCAAAAGTAGCACATCCAGACTCTGTCACTC 2940
Qy 2941 GCGTTCTGGGGGAGCTGGTGGTAACCCCTCCAGGTGGCTGGCCAGGCCACTGGCACC 3000
Db 2941 GCGTTCTGGGGGAGCTGGTGGTAACCCCTCCAGGTGGCTGGCCAGGCCACTGGCACC 3000
Qy 3001 CGCGCACTGGAAAGGCAGCTCCGAAGGCAAGGCAAGGACCTCTGACGGAAAGTCTGAGAAGG 3060
Db 3001 CGCGCACTGGAAAGGCAGCTCCGAAGGCAAGGCAAGGACCTCTGACGGAAAGTCTGAGAAGG 3060
Qy 3061 CAGGGC2ACCTCGACGCTGATGATTCCAAGGAACCTGCAACCCCTGCTG 3120
Db 3061 CAGGGC2ACCTCGACGCTGATGATTCCAAGGAACCTGCAACCCCTGCTG 3120
Qy 3121 TTCCCGAAGCCAAACGAAAGAGTCTCGAGGACCCGTGCCGCTTGGCAACACCTCTGCG 3180
Db 3121 TTCCCGAAGCCAAACGAAAGAGTCTCGAGGACCCGTGCCGCTTGGCAACACCTCTGCG 3180
Qy 3181 CTGGATGATCGTGAATTCTCTACGGCCTGCTCGAGGACACTTGTACCGCCCTG 3240
Db 3181 CTGGATGATCGTGAATTCTCTACGGCCTGCTCGAGGACACTTGTACCGCCCTG 3240
Qy 3241 CCAGATGTCGCCACCCACTGCTTCCGCTGGATCTCTGAGCCAGACATAAG 3300
Db 3241 CCAGATGTCGCCACCCACTGCTTCCGCTGGATCTCTGAGCCAGACATAAG 3300
Qy 3301 GGTATGCCAATGTTGGCCAAACGTCAACGCCAGATCCGGCCAGATCTGAGCCAGATAAG 3360
Db 3301 GGTATGCCAATGTTGGCCAAACGTCAACGCCAGATCCGGCCAGATCTGAGCCAGATAAG 3360
Qy 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCCTCCAAACAGGCCAT 3420
Db 3361 CGCTCCGTTGAGTCTGTCAACCGCAACCGCAGAAAAGGAGATTCCCTCCAAACAGGCCAT 3420
Qy 3421 GTTGCTGACCATTCGCTGGTTGTCAACCGCTGACTGTGTCAGGTGATGAGGTCAAG 3480
Db 3421 GTTGCTGACCATTCGCTGGTTGTCAACCGCTGACTGTGTCAGGTGATGAGGTCAAG 3480
Qy 3481 GCTGGAGATGCACTGCAATCATCGAGGCTATGAAAGTGAAGGCAACAAATCATGTGCTCT 3540
Db 3481 GCTGGAGATGCACTGCAATCATCGAGGCTATGAAAGTGAAGGCAACAAATCATGTGCTCT 3540
Qy 3541 GTTGACGGCAAATCGATCGGTTCTGCTGCAACGAAGGTGGCAG 3600
Db 3541 GTTGACGGCAAATCGATCGGTTCTGCTGCAACGAAGGTGGCAG 3600
Qy 3601 TTGATCGTCTGTTCTCAA 3621
Db 3601 TTGATCGTCTGTTCTCAA 3621

Query Match Score 1294.4; DB 3; Length 4403765;
Best Local Similarity 35.7%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;

Qy 238 AAGATCTGGTAGCAAAACCGGGAAATCGGGTCCGTTCCGGCAGCACTCGCAA 297
Db 3317308 AAGGTGCTGTCGCCAATCGGGGAGATCGGATCCGGCTTCTGCGCTACGAA 3317249
Qy 298 ACCGGTGCAGCCACGGTAGCTATTACCCCGTGAAGATGGGATCATTCACCGCTCT 357
Db 3317248 CTGGGGGTCGAGACCGTGGCTTACAGGACCGCAATTGGCAGACCGTCTC 3317189
Qy 358 TTTGGCTTCTGAAGCTGTCGGCATTCGGTACCGAAGGCTCACCACTGGAC 417
Db 3317188 AAGGGGAGCAGGTCTTACAGATGGGACATCGGTACCCGGTGCATGATACTGTG 3317129
Qy 418 ATCGATGAAATTATCGTGTGAGCTAAAGTAAAGCAGATGCCATTACCGGGATAAC 477
Db 3317128 GTGACGAGATGTCGCGAGATCGTGGCTGGGGATCTGGCTGGCTAC 3317069
Qy 478 GGCTTCCTGTCGAAATGCCAGCTTGGCCGAGTGTGGGATAAGTCTCCGGGATACTTT 537
Db 3317068 GGGTTCTATGGGAATTCGGGATCTGGCTGGCAAGTCTGGCTGGCTAC 3317009
Qy 538 ATTGGCCAACCCCAGAGTTCTGATCTCACGGCTGAGTGTGGGAAACGGCATTACTTT 597
Db 3317008 GTGGTCCCAGGCCAAAGTGTGGCTGGGAAATAAGTCTGGCTGGGATAAG 3316949
Qy 598 GCGAGAAGGGTGGTCTCCAGTTGGGAAATCCACCCGAGCAAACATCGATGAG 657
Db 3316948 GCCGGGAAAGCCGGCTGATGTCCTGGCTGGCGCTGGCTGAGCGAA 3316889
Qy 658 ATCGTTAAAGGCGCTGAGCTTACCCATCTTGTGAAGGGCAGTTGGGGGGT 717
Db 3316888 CTGCTGTGGTGGCCGATGCGTTCCGGCTGGTGTGTCAGGGAGTTGGCTGGC 3316829
Qy 718 GCGGAGCGGGTATGGTTTCACCTGATGAGCTTCACCTGATGAGCTTGGCT 777
Db 3316828 GGGGGGGGGTATGGCTGGGATATGGCTGGGATGGGGGATGGAGGCC 3316769
Qy 778 GCATCTGTTGAGCTGAAGGGCTTGGGATGGGGTATATGTCGAACGTTGCTGTG 837
Db 3316768 GCCAGCCCCAGGGGAGTCGGCTGGGGACCCGACGGCTTCTGGGAGCTG 3316709
Qy 838 ATTAAACCCCTGAGCATATTGAAAGTGCAGATCCTGGGATGGGGAGCTGGGAC 897
Db 3316708 ATCAATCCACGCCACATCGAGGGAGTCGGGGAGCTGGGGAGCTGGG 3316649

RESULT 3
US-09-103-840A-2/C
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A

Qy 898 CTTATGAGCTGACTGCTCACTGCAAGGATGGTCACTGGTCACTGGGAAATTGGGCCA 957
Db 3316648 CTCTATGAGCTGACTGCACTGGTCAAGGCTGGCTGGCTGGCC 3316589
Qy 958 GCACAGCATTGGATCCAGAACACTGCGTCACTGGTCACTGGGAAATTGGGCCA 1017
Db 3316588 GCGCCGCACCTGGACGCCAGTTGCGCTGGCTGGCTGGCC 3316529

Qy 1018 CGCTCCATTGGTACCCAGGGGGAAACCGTGGAAATTCTGGTCACTGGGCCA 1077
Db 3316528 CGCCCATATGGTACCCAGGGGGCAACCGTGGCTGGGCCA 3316469

Db 3314314 CTG---GAGGGTGGGGAGCTGGTATCGGGCTGGGACCGAACCGA 3314258 Qy 538 ATTGGCCAAACCCAGGGTTCTTGATCTACCGGTATAAGTCTGGGGTAACGCC 597 Db 3322734 GTCGGTCCAGGCCAACGGTGGCTGGAAATAAGTTCGGCATCGGGG 3322675

Qy 3298 AAGGGTATGCCAATGTTGGCAGACGGCCAGATCGGCCAATGGTGTGGT 3357 Db 3314257 CGGGCATGGAACGGTGTGGCATCTCAACGGCAACTGGTGAAGTGGC 3314198 Qy 598 GCGAAGAAGGCTGGTCTGCCAGTTGGGGAAATCCACCCGGAAAAACATCGATGAG 657 Db 3322674 GCCCGGAAGCGGCCTGGCGATGTCCTCGGGCTCGGTGAGCAA 3322615

Qy 3358 GACCGCTCGTGTGAAACGGCAACGGAGATCTCCCAACAGGGC 3417 Db 3314197 GACCGCAGATTGCAAGTGGCGTTCGGCGGACGGAAAGGGCAATCCCGGA 3314138 Qy 658 ATCGTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGGAGTTGCCGGTGGT 717 Db 3322614 CTGGTGTGGTGGCCGGATGCGTTGGTGTGGCTGGCG 3322555

Qy 3418 CATGTTGTCGACCCATTGCTGGTTGACTGCTGGTGAAGGTGAGTGGTC 3477 Db 3314137 CACATGCGGCCAATGCGCACCATCGGGGAGTGGGAGGGTC 3314078 Qy 718 GCGGGACGGGTTGGGTATGGCTTTGGTGTGAACGGTAAACAGAAA 777 Db 3322554 GGGGGCGGGGTATGCGTGTGGTGGGGATATGCCGGGGCTTCGGAGGCC 3322495

Qy 3478 AAGGCTGGAGATGGCAGTCAATCATCGAGGCTATGAAGAATGGAAACAATCACTGCT 3537 Db 3314077 GGCGCCCAAACCATCGCCACCATCGGGGAGTGGGAGGGTC 3314018 Qy 778 GCATCTCGTGAAGCTGAAGGGGGTTTGGGGATGGGGTATATGTCGAACGTGCTGTG 837

Qy 3538 TCTGTTGACGGCAAATCGATCGGGTTCTGCTGCAACGAAAGGTGGC 3597 Db 3314017 CCGGTTGCCAACCGTGGAGGGTGGGGTGTGGTGTGGCTGGAGGGCGGA 3313958 Qy 838 ATTAAACCTCAGCATATTGAAAGTGCAGATCCCTGGGATCACA TGAAAGTTGTACAC 897

Qy 3598 GACTTGTATGTCGTCTCGTCTCTAA 3621 Db 3322434 ATCAATCCACGCCACATCGAGGTGAGATTCTGGGGACAACCTTGGGAGCTGATCCAT 3322375

Db 3313957 GACCTGTTGGTGGGGTGTGGTGTGGCTGA 3313934 Qy 898 CTTTATGAAACGGTGAACGTGACTGCTCACTGCAGGGTCACTGGGAAAGGGCAAC 957

Db 3322374 CTCATGAGGGTGAACGTGACTGAGTGTGAGGGTCACTCGAGGCTGGGCC 3322315

Qy 958 GCACAGCATTGGATCCAGAAACTGGCTGATCGCATTGGGGATGAGTAAAGTTCCTGC 1017

Db 3322314 GCGCCGCACCTGGACGCCGAGTGGCTTCCTGC 3322255

Qy 1018 CGCTCCATTGGTACCGGGAAACCGTGGAAATTCTGGTGAAGAAAGGCCAAC 1077

Db 3322254 CGCCATATCGGTACAGCTGGTCAAGTGGTGGGAGGGAG 3322195

; RESULT 4

; US-09-103-840A-1/C

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103, 840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

; US-09-103-840A-1

Query Match 35.7%; Score 1294.4; DB 3; Length 4411529;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 3;

Qy 238 .AAGATCTTGGTAGCAAACCGGGGAAATCGGGTCCGGTGTGGCACTCGAA 297 Db 3323034 AAGGTGCTCGTGCCTAACGGGGAGATCGCGATCGGGCTTGTGGCTACGAA 3322975

Qy 298 ACCGGTGCAGCCACGGTAGCTATTACCCGGTGAAGATGGGATCATCCACCGCTCT 357 Db 3322974 CTGGCGTGGAAACCGTGGCTTACCGAGGACCGCAATTCGGACCTGGTCT 3322915

Qy 358 TTGGCTCTGAAGCTGTCCGCAATTGGTACCGAAGGCTACCTGGAC 417 Db 3322914 AAGGGGAGGAGTGTGGCTTACCGAGTGGGACATTCGGCAATGGCTAC 3322855

Qy 418 ATCGATGAAATTATGGTGGAGTCTTACCGAGTGGGACATCGGTACCTGGT 3322795

Qy 3322854 GTCGACGGAGATCGTGGGAGCTCCGGTCAACCGGTGATGGCTAC 3322735

Qy 478 GGCTTCCGTCTGAAATGCCAACCTGGCTTCAAGGCTCAGTGGGAGCTAC 537

Qy 3322794 GGTTTCTATCGGAGAATCGGATCGGGCATCGCTGGCTGGGG 3322175

Qy 1558 ATTGGCGATCACCGGACACTCTGGCTTCAAGGCTCAGTGGGAGCTAC 1617

Db 3321774 TTCTGCAAGGGTCTGTGATGACCCGGACTTCGAGGGGACTTC 3321715

Y	1618	CTGGATTACTTGGCAGATGTCAACCGCTCATGGTGTGGTCCAAGGATGTT	1677
b	3321654	CTTAACCTCTGGCCGATGTCAACCGTAAACCCGTATGGCTCGGTCAACGATC	3321595
Y	1678	GCAGCTCTTAAAGGATCTGGCTAACATCAAGGATCTGGTGTGGTTCGGT	1737
b	3321594	TACCGGACGAAAGCTGCCGATCTGCTGGGGAGATGGTGGCTGGTCAAAG	3321535
Y	1738	GACCGCTGAAGCAGCTTGGCCAGCCAGCTGGTGTGGAGGACGCCA	1797
b	3321534	CAGGGACTAGTCAAGTCAACGGTACCGATCCGGGAAAGGATTGCTACCGT	3321475
Y	1798	CTGGCAGTTACTGATAACCACCTTCCGGATGCAACCGAGCTGGTGTGG	1857
b	3321474	GTGGGGTCAACGATACCGATACCGATTCGGGATGGCTACCGTACCGT	3321415
Y	1858	CGCTCAATTGGCACTGAAGGCTCTGGCGATGGCAAGGCTTGAGCTTTG	1917
b	3321414	CGCACCAAGGGACTGTGGGGGGGGGACCGTATCTCGGGATGGCTGTG	3321355
Y	1918	TCCGTGGAGGCTGGGACTACGATGGGAGGGCAAGGGCCTCGAAGGG	1977
b	3321354	TCCGTGGAGGACTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3321295
Y	1978	CCGTGGAGCAGGGCTGGGCGGACTACGATGGGGGATGGCTCTTGAGG	2037
b	3321294	CCCTGGAAACGGGTGGCCACACTGGGTGAGCAATGGCAATGGGATG	3321235
Y	2038	CTTCGGGGCAACGGGATACCCAGACTCCGGTCTGGCGCGGTT	2097
b	3321234	TRGCGGGCAATAACGGGTGGGGGTACCGTGGTGGGGGTACCGT	3321175
Y	2098	GTTAAGGAAGGCTGCCAGCAACCGGGGATACCCGATCTTCCGAC	2157
b	3321174	GTGCAAGGAAGCAACGGCAACCGGGTATCGACATCTTGTGACGTC	3321115
Y	2158	GTCTCCAGATGCCAGTCCGGCATCTTCCGACATCTTCCGACGAC	2217
b	3321114	ATCGAGTCGATGGCTACACGGGTATCGACATCTTGTGACGTC	3321055
Y	2218	GTGGCTATGGCTTATTCTGGTGTGATCTCTGGCTCACATCTGGGAT	2277
b	3321054	GTGGGATGGCTACACGGGACCTTACCGGAGATCGTGGCTGACGGT	3320995
Y	2278	TACTACTAAAGATGGCAGGGAGATCGTCAAGTCTGGCTGGGCT	2337
b	3320994	TACTACTGAAACTGGCTGGACTGTGGCTGGAGATCGTGGCTGAGT	3320935
Y	2338	GATATGGCTGGCTGGCCAGTGGCAACCCACGGGAGCTGGGCGT	2397
b	3320934	GATATGGCTGGACTGTGGCTGGGACTGGCTGGGAGATGGCTGGGAGT	3320875
Y	2398	GAATTGGCAGCTGGCCAGTGGCACACCCACGGGAGCTGGGCAACC	2457
b	3320874	CGCTTGACCTGGCCGCTGGCACCCGGGTGGGAGATGGCTGGGAGT	3320815
Y	2458	TACTTGGCAGCTCAAGCTGGCAGATGGCTGGCATTCGGCACCCGT	2517
b	3320814	TATGTGGCCGCTGGCACCCGGGTGGGAGCTGGCTGGGAGGTGAC	3320755
Y	2578	GATAACGGGTTGAGCCTGGCCATTGGAGCTGGTGTGGGAGCGACT	2637
b	3320694	GACACGGGCTGGCTGGCATCCGGGATGGCTGGGGGTATCACCAC	3320635
Y	2638	GGACTGTACCTGGCATTGGAGCTGGCTGGCATTCGGCACCCGGCC	2697
b	3320634	AAAGTGTATGGCCGGTTCGAGTGGGGGGGGGTATCACCAC	3320575
Y	2698	GAATCCAGGGGACAGTGTCCAACCTGGTGCACAGGCCACGGCACT	2757
Db	3320574	GAGATTCGGGCAACTCATGGCAAGGAAACTACGGCCTGGTCTGGGA	3320515
QY	2758	GATCGTTTCAACTCATGGCAAGGAAACTACGGCCTGGTCTGGGA	2817
Db	3320514	GATCGATTGGTCAAGCCAACGGCTAGGGGATGGTGGCTGGGCTG	3320455
QY	2818	ACCAAGGGTACCCCATCTCCACCTCGCAGACTCCAGAACATCCC	2877
Db	3320454	GTTAAGGTCAAGCCAACGGCTAGGGTGGCTGGGACTGGCTGTC	3320395
QY	2878	GGTGTGGATCCAGGAGACTTTGGCTGGCCATCCAGACTCTGTC	2937
Db	3320394	GGTGTCACTGGAGACGAAATTGGCTCCGGATCCGGAAATCGGT	3320335
QY	2938	ATCGCGTTCTGGCGGGCTGGTAACCCCTCCAGGGGGCTGGC	2997
Db	3320334	CTCGGATTTCTGGGGAGCTGGCTGGGATCCGGGAAACGGT	3320275
QY	2998	ACCCGGGCACTGGAAAGGCCCTCGAAGGGCACCTCTGAAGGG	3057
Db	3320274	ACTCGGGGCTGGGGCCAGGGCCACT---CGTCAGGCCACCTG	3320218
QY	3058	GAGCAGGGGACCTCTGAGCTGATGATTCCAGGGCAAGGG	3117
Db	3320217	GACCGAGATTGGCCCTATCGTGGTGGAGCCAAAG---CGTCAGG	3320161
QY	3118	CTGTTCCCGAAGCCAAACGGGATGGCTGGGAGACTTTGATCC	3177
Db	3320160	TTATTCCAGTCCAAACAAAGGAAATTCAATGAGCACGGGAA	3320101
QY	3178	. GCGCTGGATGATGGTGAATTCTACGGCTTACGGGCTGGGAGACTTTGATCCGGC	3237
Db	3320100	CAATTGTCGGCCAAACCAAGGAAATTCAATGAGCACGGGAA	3320041
QY	3238	CTGCCAGATGTGGCAATGGCCACCCACTGCTGGATGGCATCTCTGAGCGAT	3297
Db	3320040	CTG--GAGCGTGGGGTGTGAGCTTCTATGGTCTGTCGAGG	3320041
QY	3298	AAGGGTATGCCAATGGTGTGGCACCCACTGCTGGGAGATCTCTGAGCGAT	3357
Db	3319983	CGCGGCATGGAAACGGGTGATGTGCAATTCCGGAAACCGGAA	3319984
QY	3358	GACCGCTCCGGCATGGCCAGTCCGGCAACGGCAACGGGAGATTCCCTCCAAACAAAGGG	3417
Db	3319923	GACCGCAGCATGGCCATTGGCAGTGGCTGCGGTAGTGGCTAGTGGC	3319924
QY	3418	CATGGTGTGGCAGGATGGCTGGTGTGGTGTGAGTGGCTGAGGGTC	3477
Db	3319863	CACATCGCCGGCCATTGGCAGTGGCTGCGGTGCGTACCGGTG	3319804
QY	3478	AGGGCTGGAGATGGCAGGATGGCTGGTGTGGTGTGGAGGTGGT	3537
Db	3319803	GGGCCGGCCAAACCATGCCACCATGGGAGATGGAAAGCCGGG	3319744
QY	3538	TCTGGTGGAGGAAATCGATGGCTGGTGTGGTGTGGAGGTGG	3597
Db	3319743	CGGGTGGCCACCCATGGGAGATGGAAAGGCGGAGGGGGGG	3319684
QY	3598	GACTTGATGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	3621
Db	3319683	GACTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	3319660
RESULT 5			
US-08-311-731A-1			
; Sequence 1, Application US/08311731A			
; Patent No. 6583266			
; GENERAL INFORMATION:			
; APPLICANT: SMITH, DOUGLAS			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES			
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR			

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 32155 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM TUBERCULOSIS
US-08-311-731A-1

Query Match 34.5%; Score 1249.6; DB 4;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 1274;

QY 238 AAGATCTGGTAGCAAACCGGGAAATCGCGGTCCGTG
Db 1574 AAGGTCTCGCCAATCGGGGAGATCGGATCCGG
QY 298 ACCGGTGCAGGCCACGGTAGCTATTACCCCCGTGAAGATC
Db 1634 CTGGCGTCGAACCCTGGCCATTATCCGTACGAGGACCC
QY 358 TTGGCTTCTGAAGCTGTCCGCATTGGTACCGAAGGGCTCAC
Db 1694 AAGGGGACGAGTTACCAAGATGGGACATCGGTCAACC
QY 418 ATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAG
Db 1754 GTGGACGGAGATCGTGGCAACGGCCGTGCGGTGGCG
QY 478 GGCTTCCTGTCGAAAATGCCAGGGTCTTGATCTACCGGTG
Db 1814 GGTTTCTATGGAGAATCCGGATCTGGCTGGCATGCG
QY 538 ATTGGCCAACCCAGGGTTCTTGATCTACCGGTGATA
Db 1874 GTCGGTCCCAGGCCGAAGTGCTTGAGCTGGCTGGAAATA
QY 598 GCGAAGGAAGGCTGGCTGCCAGTTGGGAAATCCACCC
Db 1934 GCCCGGAAAGCCGGCTGGCTGCTGATGRCCTCGGGCG
QY 658 ATCGTTAAAGGCTGAAGGCCAGACTTACCCATCTTGC
Db 1994 CTGGCTGGCTGGTGGGGGGCATGCCGTTTCCGGTGGTCG

Query	Match	Score	DB	Length
Best Local Similarity	49.1%	Score 509.2;	DB 4;	Length 3492;
Matches 1661;	Conservative 0;	Pred. No. 1.1e-134;		
Matches 1668;	Mismatches 1668;	Indels 51;	Gaps 10;	
Qy	TCAAAAGATCCTGGTAGGCAAACGGGGCAAATCGGGGTCCGTCTGGCTTTCCGTGGCAC 292			
Db	65 TGAAAAGGTATTAGT TGCCAAATCGTGGGAAATTGGGATTCAATTAGCTTGTTGTA 124			
Qy	TCGAAACCGGTGCAGCCACGGTAGCTATTACCCCCGTGAAGATCGGGATCATTCACC 352			
Db	125 CAGAATTAGATAATCCGTTACAGTAGCGATTATGCTGCAGAAGATGAGTATTCTGTTCATC 184			
Qy	GCTCTTTGCTTCTGAAAGCTGTCGGATTGGTACCGAAGGGCTCACAGTCAGGGTACC 412			
Db	185 GTTCAAAAGCAGATGAAGGGTATTAGTTGGTAAGGGAAAAACAAATGAAGCCTATT 244			
Qy	TGGACATCGATGAAATTATCGGTGCAGCTAAAGTAAAGCAGATGCATTACCGGG 472			
Db	245 TAGACATTGAAAAATATTCCAATTGCCAAATGGGAGCAGATGCCATTCTCTG 304			
Qy	GATAACGGCTTCCTGAAATGCCAACGCTTGGCCAGTGTGGAAAACGGCATTAA 532			
Db	305 GTTATGGCTTTTATCAGAGAACTTAAGCTTCAGGAAACTTACGCTTCAGGAAATCA 364			
Qy	CTTTTATTGGCCAACCCCAGGGTTCTGATCTCACCGGTGATAAGTCTCGGGTAA 592			
Db	365 TTGTCGGCTAAACACATCATTTAGATATTGCTTCAGGCTGATAAAATTAAAGGAAATCA 424			
Qy	CGCCCGGAAGAAGGGCTGGCTGCCAGTTGGGAATC---CACCCCGAGCAAAACA 649			
Db	593 425 AAGCAGCTGTAAGCTGGGGATTGCTTCAGGCTCAGACGGCCAGTAGCAACGG 484			
Qy	TCGATGAGATGTTAAAAGGGCTGAAGGCCAGACTTACCCCATCTTGTGAAGGCAGTTG 709			
Db	650 485 TGGAAAGGGTTGTAAGCTTTGCTGAAACACATGGCTTCCATCATGATTAAGCTGCTT 544			
Qy	CCGGTGGGGACGGGTAATGGGTTGCTTCACTGATGAGCTTCGGCAATTAG 769			
Db	545 TAGGTGGGGGTGGGGATGCGGCTTGGCCACGATGCCAAAGAACCGAGGAAAGGT 604			
Qy	CAACAGAAAGGCAATCTCGTGAAGGCTGAAGGGCTTTCGGCGATGGCGGTATATGTCGAAC 829			
Db	770 605 ACGAAAGGGAAAAGTGAAGCGAAAGCAGCCTTGGTCTGACGAGGTTATGTTGAAA 664			
Qy	GTGCTGTGATAACCCCTCAGCATATTGAAGTCAGATCCTGGGATCACACTGGAGAAG 889			
Db	830 665 AGTATATTCTTAATCCTAATCGAAGTACAATTGAGTCAATTGCGGATCATGGGAACG 724			
Qy	TTGTACACCTTATGAAACGTGACTGCTCACTGCAGGCTCGTCACCAAAAGTTGTCGAAA 949			
Db	890 725 TCTTGCAATTGTAACGTGATTGTCAGGCTTCAACGGCCACCAAAAGTGGTAGAAAG 784			
Qy	TTGCCAGCACAGCATTGGATCCAGAACCTGGTGAATTGTGGGATGCCAGTAA 1009			
Db	950 785 TCGCACCATGTTGATCAATGAAATGAAGAACAGGAGCCATTGTTCTGCTGTGC 844			
Qy	AGTTCTGGCCATTGGTACCGGGCAACCCAGTATCCAGGTGATTCAGGTGAAATTCCTGGGAAACCGGTGACTG 11069			
Db	1010 845 AGTTAATGGCACATGTCGGCTACGTGAATGCGGAAACGGTTGAGTTTAGT--AGAAG 901			
Qy	AAGAAAGTACCCGAGGTGGACCTGGTAGGGGAAACCGGTGAAATTCTTGGTCGATGAAA 1189			
Db	1130 962 AAATGATTACAGATATTGATATTGCTCAATTACAATAGATAAGGCTTGATT 1021			
Qy	AGGGCAACCAACGTCTCATGAAATGAAACCCAGTATCCAGGTGACCGCACTG 1243			
Db	1190 902 GGGATCAGTTTATTGAAAGTGAATCCCTCGTGTTCAGGTAGAACATACTACACAG 961			
Qy	TGAAGGAA-----TGGGCTCTGACCCAAAGATAAGATCAAGACCCACGGTGCAGCACTGC 1129			
Db	1022 TGCATAAAGATATGCCATTGCAAAACAAAGAACATTAAAGGGCTTATTTC 1081			
Qy	AGTGGCCGATCACCAACGGAAAGATCCAAACAAACGGCTTCGGCCAGATACCGGAACCTCA 1303			

b	1082	AATGTCGGATTACGACTGAAGATCCCTGAAACAGTTATGCCAGACACAGGAAATCG	1141
y	1304	CCGGGTACCGCTCACCAAGGGAGCTGGCGTTCGCT---TGACCGGTGCAAGCTCG	1360
b	1142	ATACGTATCGTTACCAAGGTGGTTAGATGTAGGAATGCTTATTCTCG	1201
y	1361	GTGGGAAATCAGGACACTTGACTCCATGCTGGCACAGCGCGTTGGCTCACCGTGTCTGGT	1420
b	1202	GCTACGCTGTGACTCCCTACTTGTATTGTTAAAGTCTGATGGTTCT	1261
y	1421	ACTTTGAAACTGCTGTTGCTGCACAGCGCGTTGGCTCACCGTGTCTGGT	1480
b	1262	CTTTGAAACAGGCAATCAGTAATAATGCAACGCTGCTTAAGAATTTCGGATTCTGGGG	1321
y	1481	TGGCAACCAACATTGGTTCTTGGCTGGGGAAAGAGGACTTCACTCCAAGC	1540
b	1322	TGAAAACAAATATTCCGGTTTACAACCTGAGCTATCCAGCGTTCAATCTGGCG	1381
y	1541	GCATCGCCACCCGATTCACTGGCGATCACCCGACCTCCCTCAGGCTCCACCTGCTGATG	1600
b	1382	AAGCCAAACACCTTATTGATAATAACACCTGAAATTTCCTCGTATGGCG	1441
y	1601	ATGAGCAGGGACGGATCTGGATTACTTGGCAGATGTCACCGTGAACAGCCTCATGGT	1660
b	1442	ATCGTGGCAATAAACGATGAAATAACATGGAGAAGTAACGGTCAAATGGGTTCCCTGGCA	1501
y	1661	TGGTCAAAAGGATGTTGCGAGCTCCCTATCGATA-----GCTGCCTAACATCAAGGATC	1714
b	1502	TGAAAGAACGGAGAAAAAATATTGAGCCCCGGCTGCCACAGATAATTGAAGGTT	1561
y	1715	TGCCACTGCCACGGGTTCGGCCTGAAAGCAGCTGGCAGTTACTGATAACCACCTTCCGGATGCCACCC	1774
b	1562	CAGAAAAAGTGAATTACAGCTAAATAATTCTAGACGCTCAAGGAGCAACCGGTCAATCG	1621
y	1775	GTGATCTCGTGGCAGGACGGCAACTGGCAGTTACTGATAACCACCTTCCGGATGCCACCC	1834
b	1622	ATTGGGTTAAGAATCAAGAAAGTGTGTTAATGACAGATAACCAGTTCCGTGATGCCAC	1681
y	1835	AGTCTTGGCAGCCGGAGTCCGCTCATTCGCACTGAAAGCCTGGCAGGGCGTGTG	1894
b	1682	AAAGTTTATTAGCTACTCGTGTGAGAACACAAGATTAAAGCAATTGCTGGTCTAACTG	1741
y	1895	CAAAGCTGACTCCTGAGCTTTCGGAGGGCCTGGGAGGCGACTACGATGTTG	1954
b	1742	ATGCAGCCCTGGCTGAGCTGTTCTACTGAAATGTGGGTGGCTACGTTTCGATGTTG	1801
y	1955	CGATGCCTTCTCTCGTGGGACAGGGCTCCAGGAGCTGGGATAACCCCGTACCGGTGCTGC	2014
b	1802	CCTATCGCTTCCTTAACCGAACCCATGGCAACGTTAAGAAAATTCTGTCAGTTGATGC	1861
y	2015	CGAATGTAACATTCAAGATGCTGCTTCGGCCAAACACCGTGGGATAACCCCGTACCGGTGCTGC	2074
b	1862	CAAAACACACTTTACAAATGCTGTTCAAGGGATCTAATGGCTATAAAATTATC	1921
y	2075	CAGACTCCGTCGGCGTTGTTAAGGAAGCTGCCAGCTCCGGCGTGGACATCTTCC	2134
b	1922	CTGATAATGTTATTGAGAAATTAAAGAATCCGCTGCCAAGGAGTCGATGTTTTC	1981
y	2135	GCATCTTCGACGGCTTAACGACGCTCCAGATGCGTCCAGAAATCGACGGCAGTCCTGG	2194
b	1982	GAATTGGTGAATAGCTTAAACTGGATTCCTCAAATGGAAAAGTATTCAAGTCCAG	2041
y	2255	ATGAAAAGCTCTACACCCCTGGATTACTACCTAAAGATGGCAGGGAGATCGTCAGTCTG	2314
b	2042	ATACCGGAA--AAATTGGGAAGCAGCAATTGTTATACTGGGACATCAATGATCCAG	2098
y	2099	CCCGAGCAAAATATAATGTTCAATACCTGCTAAAGAATTGGAAAATTATTTAG	2158
y	2315	GGGCTCACATCTGGCCATTAAGGATAAGCTCTGCTTCGCCCCAGCTGGGTAACCA	2374

Db 2159 GTGCACAAATCATTGGGATTAAGATAATGGCTGGCTTATTGAAACCACAAAGCTTGCTTATC 2218 Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 Qy 3551 AAATCGATCGCTTGTGGTT 3 570 Db 3416 CGGTAGATCACATTATGTT 3 435

Db 2399 ATGCTTGTCAATGGTGAACGGACCAACTTCCCTGCTGCCATTGGTAAATGCC 2458 Qy 2615 AGCCGTACTGGAAAGCAGTGGCAGACTGTGACTCTGCCATTGGAGCTGGAAACCCAGGCC 2674 Db 2459 ATCATTATTGGAAAGATGTGCGATGTGAGTCAACATTGAAATGGTTAAATGCC 2518 Qy 2675 CAACCGGTGGTGGTCTAACGCCAACGAAATCCCAGGGAGCAGTTGTCACCTGCCAACCTGGCAC 2734 Db 2519 CGCAAACAGAAGTCTATATGCCATGAATGGCTGGGAAATACTCTAACAGGCC 2578 Qy 2735 AGGCCACCGGACTGGGCCCTGGGATCCTCAACGGAAACTACGCCAGCC 2794 Db 2579 AGCAAAAGGGTAGGGCTTGGGACCCCTTGGGATGAAATCAACACAG 2638 Qy 2795 TTAATGAGATGCTGGGACGCCAACGGTCAACCTCACTGGTGGGGGACC 2854 Db 2639 TGAATTGATGTTGGGATATTGTAAGTGAACATCAAAAGTGTGGGAGACA 2698 Qy 2855 TCGCACTCACCTCGTGGGGTAGCCAGCAACTTGGCTGCCGATCCACAAA 2914 Db 2699 TGGCACTCTTCATGGTTCAAAATAATCTGACAGAACAGATGTTATGCGCTGGTGGAAAG 2758 Qy 2915 AGTAGCACATCCCAGACTCTGTCACTGGTCTCCTGGGGAGCTTGGTAACCCCTCCAG 2974 Db 2759 ACTAAGTTTCCTGAATCAGTTGTGACTTTCAAAAGGTCAACCCAGTTG 2818 Qy 2975 GTGGCTGGCCAGAGCAGCCACTGCGOACCCGGCACTGGAAAGGGCGCTCCGAAGGGCAC 3034 Db 2819 GTGGGTTCCGAAAGAGGTGCAACGAATTATTCTAAAGGTGACCCCTTOACAGAGC 2878 Qy 3035 CTCTGACGGA--AGTTCTGTGAGGAAGGGAGGGCACTCGACGCTGATGATTCACGG 3091 Db 2879 GGCCAGGTGACTTGGCACCTGGGATATTGTAAGGAGAAATTAGCCGAAA 2938 Qy 3092 AACGTCGAATAGCCTAACCGCC-----TGCCTTCCGAAAGCCAA 3133 Db 2939 AAATTGGGATCAACTAAATTGGAAGAAGTTAAAGTTATTAAAGTATCCAAAGTAT 2998 Qy 3134 CCGAAGAGTTCTCGAGCACCGTCCGGCAACACCTCTGGCTGGATGATCGTG 3193 Db 2999 TTGTTAGAGTATGGTCAAAAATACGAAACCTTGGAGATAATAACCTTATTAGATAACGCCAA 3058 Qy 3194 AATTCTCTACGGGCTGGTGAAGGGCCAGACTTGGATCCGCAAGTGTGGCA 3253 Db 3059 CATTCTTAAATGGTCAAGGA--GAGACATTGGAAATTGAAAGGGAA 3115 Qy 3254 CCCCACTGCTTGGGATGGCACTCGCCAGATCCGGCTGGGAGACTTGGATCCGGCT 3313 Db 3116 AACGTTAAATTCTGTTAGATGAAATTGGCAACCTGATATTGACGAAACCGTGTCT 3175 Qy 3314 TTGGGCCAACGTCACGGCCAGATCCGCCAATGGCTGGTGAACGGCTCGGTGAGT 3373 Db 3176 TGTCTCAATTGATGGCAACGTCGTGAGGTTTGAAGTAAAGTGCCTTAAAGT 3235 Qy 3374 CTGTCACCGGCAACCGAGAAAAGGCAGATTCTCAACAAAGGGCAATGTTGCTGCACCAT 3433 Db 3236 CTGCTGTTCAAGTAAAAGGGAAACCAACTAAAGAACAAATCGGGCAACGA 3295

RESULT 7 US-09-134-001C-591 ; Sequence 591, Application US/09134001C
Db 2399 ATGCTTGTCAATGGTGAACGGACCAACTTCCCTGCTGCCATTGGTAAATGCC 2458 ; Patent No. 6380370
Qy 2615 AGCCGTACTGGAAAGCAGTGGCAGACTGTGACTCTGCCATTGGAGCTGGAAACCCAGGCC 2674 ; GENERAL INFORMATION:
Db 2459 ATCATTATTGGAAAGATGTGCGATGTGAGTCAACATTGAAATGGTTAAATGCC 2518 ; APPLICANT: Lynn Doucette-Stamm et al
Qy 2675 CAACCGGTGGTGGTCTAACGCCAACGAAATCCCAGGGAGCAGTTGTCACCTGCCAACCTGGCAC 2734 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
Db 2519 CGCAAACAGAAGTCTATATGCCATGAATGGCTGGGAAATACTCTAACAGGCC 2578 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
Qy 2735 AGGCCACCGGACTGGGCCCTGGGATCCTCAACGGAAACTACGCCAGCC 2794 ; FILE REFERENCE: GTC-007
Db 2579 AGCAAAAGGGTAGGGCTTGGGACCCCTTGGGATGAAATCAACACAG 2638 ; CURRENT APPLICATION NUMBER: US/09/134,001C
Qy 2795 TTAATGAGATGCTGGGACGCCAACGGTCAACCTCACTGGTGGGGGACC 2854 ; CURRENT FILING DATE: 1998-08-13
Db 2639 TGAATTGATGTTGGGATATTGTAAGTGAACATCAAAAGTGTGGGAGACA 2698 ; PRIOR APPLICATION NUMBER: US 60/064,964
Qy 3092 AACGTCGAATAGCCTAACCGCC-----TGCCTTCCGAAAGCCAA 3133 ; PRIOR FILING DATE: 1997-11-08
Db 2939 AAATTGGGATCAACTAAATTGGAAGAAGTTAAAGTTATTAAAGTATCCAAAGTAT 2998 ; NUMBER OF SEQ ID NOS: 5674
Qy 3134 CCGAAGAGTTCTCGAGCACCGTCCGGCAACACCTCTGGCTGGATGATCGTG 3193 ; SEQ ID NO 591
Db 2999 TTGTTAGAGTATGGTCAAAAATACGAAACCTTGGAGATAATAACCTTATTAGATAACGCCAA 3058 ; LENGTH: 3465
Qy 3194 AATTCTCTACGGGCTGGTGAAGGGCCAGACTTGGATCCGCAAGTGTGGCA 3253 ; TYPE: DNA
Db 3059 CATTCTTAAATGGTCAAGGA--GAGACATTGGAAATTGAAAGGGAA 3115 ; ORGANISM: Staphylococcus epidermidis
Qy 3254 CCCCACTGCTTGGGATGGCACTCGCCAGATCCGGCTGGGAGACTTGGATCCGGCT 3313 ; US-09-134-001C-591
Db 3116 AACGTTAAATTCTGTTAGATGAAATTGGCAACCTGATATTGACGAAACCGTGTCT 3175 ;
Qy 3314 TTGGGCCAACGTCACGGCCAGATCCGCCAATGGCTGGTGAACGGCTCGGTGAGT 3373 ;
Db 3176 TGTCTCAATTGATGGCAACGTCGTGAGGTTTGAAGTAAAGTGCCTTAAAGT 3235 ;
Qy 3374 CTGTCACCGGCAACCGAGAAAAGGCAGATTCTCAACAAAGGGCAATGTTGCTGCACCAT 3433 ;
Db 3236 CTGCTGTTCAAGTAAAAGGGAAACCAACTAAAGAACAAATCGGGCAACGA 3295 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCGATCGCTTGTGGTT 3 570 ;
Db 3416 CGGTAGATCACATTATGTT 3 435 ;
Qy 3434 TCGCTGG---TGTGTCACCGTGACTGTTGACTGAGGTGATGGCTGGAGATG 3 490 ;
Db 3296 TGTCGGTCTGTTCAAGTATTGGTCAAACGTGGGATAAAGTAGAAAAGGTCAAGC 3355 ;
Qy 3491 CAGTCGAATCATCGAGGCTATGAAGATGGAAGAACAAATCAGTGTTCTGTTGACGGCA 3550 ;
Db 3356 CGTTGCTGATTACAGAACGCAACTATGAAATGGAAACGACTATGAAAGCATGAAAGGGCA 3415 ;
Qy 3551 AAATCG

Db	504	AAGCGGGTGGGGTAAAGGTATGCCAATCGTTCTGAAAGCTGAAGCGCTTTCGGGATGGCGTAAAGCAATTAGAACGCC 563	Db	1581	TGTTACAAATTGGGTTAGAGAACANGAAGATGTTTAAATTACCGATACTACATTAGAGA 1640
Qy	768	AGCAACAGAACCTCTGTGAAGCTCATGGCGGTATATGTCGA 827	Qy	1827	TGCACACCGTCTTGCCTGAGCTCCGAGTCATTGCAAGCCTGCGCAGA 1886
Db	564	TTCCCATGTGCGAAATCGAAGGCCAAAAGTCATGGTAATAGCGAAGTTATATCGA 623	Db	1641	TGCACACCAACTCTTACTTGCAACACGTGTAAAGAACATGTCATC 1700
Qy	828	ACGTGCTGTGTTAGTAAACCCCTCAGCATATTGAAGTGCAGATCCTGGATCACACTGGAGA 887	Qy	1887	GGCGCTGGCAAAGCTGACTCCTGAGCTTTGTCGGAGGCCTGGGGCGGCACCTA 1946
Db	624	AAGATATATTGATAATCCAAGCATATAGGGTTCAAGTTATTGGTGTAAATTGGGAA 683	Db	1701	TAAAACTGCTGAAGTTAAAGATAAGTTTCAATTAGAAATGTGGGTGCAACATT 1760
Qy	888	AGTTGTACACCTTATGAAACGTGACTGCTCACTGGAGTCGTACCCAAAAGTTGTGCA 947	Qy	1947	CAGATGGCGATGCGTTCTCTTGGAGATCCGGTGGAGACAGGCTGAGAGCTGGCGA 2006
Db	744	AGTGTGACACCTTCAGTAGGTCTTCTAAACAATAGGGTACAAAGACGTCAATGGTGTGA 743	Db	1761	TGATGTGCGCTATAATTCTGAAAGAGAATCCATGGGAAAGCTTAAAGTGGGAA 1820
Qy	948	AATTGGCCAGCACAGGATTGGATCCGAAACTGGTGTGATGGATGGCAGT 1007	Qy	2007	GGCGATGCCAGACTCCAGATGCTGCTTCGGGGCGGCAACACCCGGGATACAC 2066
Db	804	TCAACTGTGAAATAATAACGTCAACGTGGTAACTGGTGAACAGTAAAGGGAATTGGTGTGA 862	Db	1821	AGCCATTCCGAAATGGTTATTACGAGCTTCGAAACTGGTAGTTATAAA 1880
Qy	1008	AAAGTTCTGCCCTCCATTGGTATTCCAGGGGGGAAACCGTGGAACTCTGGTGTGA 1067	Qy	2067	CCCCTACCCAGACTCCGTCTGCCGGGCTGGGGTGTAAAGGAAGCTGGCGTGGGA 2126
Qy	804	-GGGATGTAATTTCCTCATGGTTAAATCCACGTGAAAGCTGAACTAACATTAC 920	Db	1881	AAACTATCCGATAATGTAATTAAAGAAATTCTGTTCATGAAAGCTGGTAGA 1940
Qy	1068	AAAGGGCAACACCACGTCTCATGAAATGGGAAACCCACGTATCCAGGTTGAGCAC 1127	Qy	2127	CATCTTCGGCATCTTCGACGGCTTAACGACGTCTCCAGATGGCTCAGCAAGCC 2186
Db	863	-GGGATGTAATTTCCTCATGGTTAAATCCACGTGAAAGCTGAACTAACATTAC 920	Db	1941	TGTTTTCGTTATTCGACTCATGAAATGAAAGTAGGGAATGGAA 2000
Qy	1128	TGAAAGAAGTCACCGAGGACCAACACCCGCGTAGCCGAGCTGGCT 1187	Qy	2187	AGTCCTGGAGAACACCCGCGTAGCCGAGCTGGCTATTCTGGTGTATCTC 2246
Db	921	TGAAATGATTACTGGTATAGACATTGTGAAAAACGCAAAATTGGAGAACATC 980	Db	2001	TGTTCAAGAAGCTGGAAATGGTATCTGAGGTACAAATTGCTGATAATTAAAA 2060
Qy	1188	CTTGAAGGAATTGGCTGTGACCTTCAAGAACCCACGGTGGCAGC 1238	Qy	2247	TGATCCAATGAAAGCTCTACACCTGGATTACTACCTAAAGATGGAGGAGATGCTG 2306
Db	981	GTTATTGGAGATAAAATCTATGCCAACAAACATTAGGTATGCA 1040	Db	2061	TGCTGAACGTCCBATAATTAGTTAGATTACGTTAAAGAAACTGGGA 2120
Qy	1239	ACTGCAGTGGCGCATCACCAGGAAGATCCAAACAAAGGCTTCGGCCAGATACGGAAC 1298	Qy	2307	CAAGTCGGCGTCACATCTGGCATTAAAGGATATGGCTGCTGCTTCGCCCAAGCTGGCTGC 2366
Db	1041	GATACAATGTGTATAACACTGAAGATCTACTAAATGATTGTTATGCCAGATCTGGAC 1100	Db	2121	AAGAGAAGGATTCCCATATATTAGCAATTAAAGGATATGGCTGTTATGAAATTCCAAATAC 2180
Qy	1299	TATCACCGCGTACCGCGTGGCTGGCTGGCTGCTGACGGTGCAGCT 1358	Qy	2367	GGTAACCAAGCTGGTACCGGCACTGGCCACTGCTGCACTGTCAGTGCACAC 2426
Db	1101	AATTATTGCAATCGATCAAGTGGGGTTGGTGTGAGACTTGTGAGGGATGGAT 1160	Db	2181	AGCTTACGAAATTAGGTGAATTACGTGAGGGAAACACATCTCCAAATAC 2240
Qy	1359	C---GGTGGGAATTCAACCGCAACTTGTGACTCCATGCTGGTGAAGAAATGACCTGCCGGTGG 1415	Qy	2427	CCAGCACACTGGGTGGCCAGCTGGCACCACCTGCTGGCAGCTCAAGCTGGCGA 2486
Db	1161	CCAGGGTGCAGAAATTTCACCTTACCTACTACGATTCACTTAAAGCTTACACATGC 1220	Db	2241	ACATGATACTAGTGGAAATTGGATTGTCACATAAAACAGCAATTGTCGGGTGATA 2300
Qy	1416	TTCGGACTTTGAAACCTGCTGTGCTGGCACAGCGGGAGCTGGCTGAGTTCAACCGTGTCT 1475	Qy	2487	TGCTGTGAGGTGCTGGCTGGCCACTGCTGGCAGCTGGCTGCTGCTGC 2546
Db	1221	CGTTTCATTAAACAAAGCTGAAGAGAAATGGAAACGTCAATTACCGAAATTGCA 1280	Db	2301	TATTATAGATACTGCTGTGATCTATGAGTTAACGAGTTAACCAAGTGC 2360
Qy	1476	TGGTGTGCAACCAACTTGGTTCTGGCTGGCTGGTGTGCGGGAAAGGGACTTCACRTC 1535	Qy	2547	CATTGTTGCTGCATTCGGGCAGACCCCGTGGGATACCGGTTTGAGCCCTCGAGGCTGTTTC 2606
Db	1281	TGGCGTAAGACGAAATTCCATTTCTCATCAATGTTATGATAAAATTAGAAG 1340	Db	2361	ATTATTATTGCACTAAATGGATTTCACGTAATTAAAGAAACTGATAATTGAGTGTAGA 2420
Qy	1536	CAAGGGCATGCCAACCGGATTCAATTGCCACCCGCCACCTCCCTAGGCTCCACCTGC 1595	Qy	2607	TGACCTCGAGCCGTACTGGGAAAGCACTGCTGGCTTACCGCCACGAGCTGGCTGGAAAC 2666
Db	1341	TGGTGTATTAACCTAAATTATTGAAAGAACACTGTAATTGCTGATATTGCCGAC 1400	Db	2421	AGAGTGTGAGTCATTACTGGCTGTGATCTGAGCTTGGCAATATTCAAAACTT 2480
Qy	1596	TGATGTGAGCAGGGACGCACTCTGGGATTCACTTCATCAATGTTATGCTGAACTTGC 1655	Qy	2667	CCAGGGCCAAACGGGCCACGGCACTGGCTGGCTTACCGCCACGAGCTGGCTGGAAAC 2726
Db	1401	ATTGGACAGAGGTACCAAGACTTTAGAGTATATTGTAATGTCATAAGCTAACATC-- 1707	Db	2481	CAAAATCCAAATACAGAAATTATCAACATGAAATGCAAGTAAAGTCAAAAGAGATGTA 2540
Qy	1656	TGGTGT-----GGCTCCAAAGGATGTTGCCATCTGGCTCCTATGTCATAAGCTAACATC-- 1707	Qy	2727	GGTGCACAGGCCACGGCACTGGCTGGCTGGCAATCTGAGCTGGCAACACTCATCGAAGAAC 2786
Db	1461	TAATGTGAAAAAGGTTAAACCCAGAATTGAAATCTACCAAAATTCTCA 1520	Db	2541	AAGTCACAAAGCTAAAGTAAAGTTAGGTTGGAGATCTTGTGAACTCTCAAAAGGTAGTA 2600
Qy	1708	-AAGGATCTGCCACTGCTGGCTGGCTGAGGAGCTGGCTGGGGGAACTGGCTGGGG 1766	Qy	2787	CGCGGACCTCGCACTCCACCTCGTTGGGGAGCCATCCTCCAAAGGGTTGTGCGCGA 2846
Db	1521	AARGAAATCAATGCAATTGCTGTTATTGGAAACAAATTCTGAGCAACATGGGAAACAGG 1580	Db	2601	TGTCGTGTCACCTCTGGTAAAGTAACCCATCTCAAAAGGTCAATCAATGTA 2660
Qy	1767	GTTTGTGCTGTGATCTCCGTGAGCAGGGACGGCACTGGGACTTACCTGATAACCGTCAATGTA 1826	Qy	2847	TGCGGACCTCGCACTCCACCTCGTTGGGGAGCCATCCTGGCTGGGG 2906
Db	2661	TGAGGATATGGCACTATATGTTGATAAGATACTGGTCAAATGTCATCAATGTA 2720	Db		

RESULT 8
US-08-956-171E-324/C
; Sequence 324, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA

QY 2907 TCCACAAAAGTACGACATCCAGACTCTGGTCACTGGGTCTGGGGAGCTGGTAA 2966
Db 2721 TGGTTATAATTAGATTCCAGAATCTGGTCATTCTTAAAGGTGACATGGACA 2780
QY 2967 CCCTCAGGTGGCTGGCCAGAGCCACTGGCACCGGACTGGGAAGGGCGCTCCGAAGG 3026
Db 2781 ACCTGTCAAAGGATTCAAAGAAATTGCAAGATGTTATTTTAAAGGACAGCAACCAAT 2840
QY 3027 CAAGGCACCTCTGACGGAAGTCCCTGAGGAAGGCGAACCTCGACGCTGATGATTG 3086
Db 2841 TACTGAAAGGACCGGGTAATACTTGAGCCGGTCAAGGAACTGGCTGATGTTCCC 2900
QY 3087 CAAGGA---ACAGGAAATTGCAAGATGTTATTTTAAAGGACAGCAACCAAT 3125
Db 2901 AGGGACATAACAAAGGAGGTAACAGAAACAAAGATAATTAGTATGACTTTATCC 2960
QY 3126 GAAGCCAACCGAAGAGTTCTCGAGGACCGTGGCCAAACACCTCTGGGTGGA 3185
Db 2961 GAAGGTATAAACAAATTATTCAAACGAAAGGCAATTGGTAATGTATCTTACTGGA 3020
QY 3186 TGATCGTGAATTCTCTACGGCTGGTGAAGGGCGGAGACTTGTATCCGCTGCCAGA 3245
Db 3021 TACACCGACATCTTATGGCATGCTTAATG--GTGAAACAGTTGAATGAAATTGA 3077
QY 3246 TGTGGCAACCCACTGCTGGTGGATGGATCTTGAGCCAGACGATAAGGGTAT 3305
Db 3078 TACTGGTAAACGTCATAATTAAATTAGAACATCTGTAATGAAATTGTTAA 3137
QY 3306 GCGCAATGGTGTGGCAACGTCACGGCCAGATCCGCCAATGGGTGCGTAGCGCTC 3365
Db 3138 GCGTACAATTATTAGCTATGTAATGGTCAAGGAAAGACTATCTATTAAAGTAAAA 3197
QY 3366 CGTGAGTGTGTCACCGCAACCCGAGATACTCCAAACAGGGCCATGTTGC 3425
Db 3198 TGTTAAACGAATGCTTAATGTTAAACCTAACATTCAATTTATGG 3257
QY 3426 TGCACCATCGCTGGTGTCA---CGTGAATCTGGTGTGAAGGTGATGAGGGC 3482
Db 3258 GGCTCAAATGCGCTGGTCTGTAACTGAAGTCAAAAGTTCAAGC 3317
QY 3483 TGGAGATGCGATCGCATACTCGAGCTATGAAAGATGAAACAAATCACTGTTCTGT 3542
Db 3318 TAATCAGCATTATTAAATCACTGAAGCAATGAAAGGAAACGATTCAAGCACCATT 3377
QY 3543 TGACGGCAAAATGATCGTGGTCCCTGTCGAACGAAGGTGGAAGGTGGGACTT 3602
Db 3378 TGATGAAATTAAACAAATCAATGGAGATGCTTAATGGAGATGCCACAGGAGATT 3437
QY 3603 GATCGTGTGCTT 3615
Db 3438 ATTAGTGGAAATT 3450

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 5030 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 324:
US-08-956-171E-324
Query Match 13.3%; Score 479.8; DB 4; Length 5030;
Best Local Similarity 48.3%; Pred. No. 3.3e-126;
Matches 1657; Conservatve 0; Mismatches 1722; Indels 54; Gaps 9;
Qy 231 ATTCAAAAGATCTTGGTAGCAACCGGGGAAATCGGGTCCGTCTTCCGTGAGC 290
Db 3846 AATAAAAAGTTACTTGTGCTAACCGTGGAGAAATTGCAATTCTGATATTAGG 3787
Qy 291 ACTGAAACCCGGTGCAGCACGGTAGGTATTACCCCCGTGAAGATCGGGATCATCC 350
Db 3786 GGCAGAAATTAGACATCAGCACAGTTGCAATTTCGAATGAAGACAAAAGTTCA 3727
Qy 351 CGCGCTCTTTGGTTCTGAAGCTGTCGCCATTGGTACCGAAGGCTCACCGTCAAGGGTA 410
Db 3726 TAGATAAAAGCAGATGAACTCTTATTAGTTGGAAAGTGTATTAGGTCAATCC 3667
Qy 411 CCTGAGCATCGATGAATTATCGGTGAGCTAACATTGGCTAACGGTCAAGGGTA 470
Db 3666 TTAAATATTGAGGTATCATTGATGTGCAAAAGCGAATGTGGATTCATCC 3607
Qy 471 GGATACGGCTTCCCTGTGAAATGCCAGCTGCCAGGTTGGGAAACGGCAT 530
Db 3606 TGGCTATGGATTTTAAAGTGAACAAATTGGCTAACATTGGAGATGCCACAGGAAAT 3547
Qy 531 TACTTTTATTGGCCAAACCCAGGGTCTTGATCTCAGGTGATAAGTCTGGGGGT 590
Db 3546 TAATTTATTGGCTCATTTAGATACTGGTAAAGTAAAGCTCG 3487
Qy 591 AACCGCCGGAAAGGGCTGGCTGGCAAGGGCAACAT 650
Db 3486 TACAGGGCTATCAAGGCAAGATTACAGTTCTGGTACAGACGGTCCAAATTAAATC 3427
Qy 651 CGATGAGATGCTTAAAGGGCTGAAGGGCAGC---TTACCCCATCTTGTGAAGGGCAGT 707
Db 3426 ATATGAATTAGCAAAAGAATTGGTCAATGATTAAAGGTGAAATGATGC 3367
Qy 708 TGCCGGTGGTGGGACGGGGATGGGTATGGCTTTCACCTGATGAGCTTCGCAAAATT 767
Db 3366 AACGGTGGCGGGTAAGGTGAAATCGTCGTGAAGAAAGTGAATTAGAAGATG 3307
Qy 768 AGCAACAGAACATCTCGTGAAGCTGAAGGGCTTCGGGATGGCGGTATATGTCGA 827

Db	3306	TTCATAGACCAAAATCAGAACCTGAAATACTTGGTAATAGTGAAGTTACATAGA	3247	QY	1887	GCGCGTGCAGAACGCTGAAACTGCCTGAGCTTGTCCGTTGAGCTTGTGGGGCGGCGACCTA	1946
QY	828	ACGTGCTGATTAAACCTCTAGGATATTGAAAGTGCAGATCCGGGATCACACTGGAGA	887	Db	2169	AAAACAGGGACGTATTAAAGATGGTTTCTCACTAGAAATGTGGGGTGTACATT	2110
Db	3246	AAGATACATTGATAATCCAAGGATATTGAAAGTACAAGTCATAGGTGACGAAACATGGAAA	3187	QY	1947	CGATGTGGGAGTCCGTTCTTCACTGGGATCCGGTCAAGGGCTCGACGAGCTGGCGGA	2006
QY	888	AGTTGTACACCTTTATGAAACGTGCTCACTGGCGTCAACCAAAGTGTGCA	947	Db	2109	TGATGTGGCATATAATTCTTGAAAGAAACCCTATGGGAAACGACTTGAACGTCTACGTAA	2050
Db	3186	TATCGTACACTTATTGAAACGTGATTGGTAGTCAACCGTGTCAAAAGTGTGATA	3127	QY	2007	GGCGATGCCGAAATGTAACATTCAAGATGCTGGCTTCGGGGATACAC	2066
QY	948	AATTGGCCAGCACAGCATTGGATCCAGAAACTGGCTGATCGCATTGTGGCGATGCACT	1007	Db	2049	AGCTTACCTCAAAATGTTACGTGTTACGTGCTTCAAACGAGTGGTATAA	1990
Db	3126	AGTTGCACCATCAGTGGATTATCATCAACATTACGTCAACGTATTGTGATGCTGCAAT	3067	QY	2067	CCCGTACCCAGACTCCGTTCTGGCCAGCTGGCTTGTAAAGGAGCTGGTGGGA	2126
QY	1008	AAAGTTCTGCCCTCATGGTACCGGGCGAACCGTGGATTCTTGTGATGAG	1067	Db	1989	AAACTATCCTGATAATGTATTCAAAATTGTACAAGAAAGTGTAAAGGATAGA	1930
Db	3066	TCAATTGATGGAAAATTAATTATGTCAATTGCAAGGTACTGTGATTCTAGTGT-	3008	QY	2127	CATCTTCCGCATCTTCGAGCGGCTTAACGACGTTCTCCCGAGATGGCTCAAGCAATGCGC	2186
QY	1068	AAAGGGCAACCAACGCTTTCATCGAAATGAAACCCACGTTACCGGTGAC	1127	Db	1929	TGCTTTAGAATTTCGATTCAATTAAACTGGTAGATCRAFTGAAAGTGGCAAG	1870
Db	3007	--GTGACCGATTCTCTTTATAAGGTTAACCCCTCGTGTACAAGTAGGATAATTAC	2950	QY	2187	AGTCTGGAGACCAACACGGGGTAGCCGGGGTATGGCTTATTCTGGTGTATCTCTC	2246
QY	1128	TGAAAGACTCACCGAGGTGGACCTGGTGAAGGGCAAGATGGCTTGGCTGGTGAAC	1187	Db	1869	AGTACAAGAACGGGGCAAAATCTCAGAAGGTACTATTGTATACAGGTGACATTAAA	1810
Db	2949	AGAGATGGTAACAGGAATTGATAATTGTTAAAGACACAAATTAGTGAAGGGTGC	2890	QY	2247	TGATCCAAATGAAAGCTTACACCCCTACACTAAAGATGGAGAGGAGATCGT	2306
QY	1188	CTTGAAGGAAATTGG-----GTCTGACCCAAAGATAAGATCAAGGTCAGGTCAGC	1238	Db	1809	TCCTGAGGGATCAAAACATTAAACTTTAGAGTAACTTAAAGGTTAGA	1750
Db	2889	TTTATTGGTGAAGAGATAAAAGATAATTACAAACATTAGGTATGC	2830	QY	2307	CAAGTCTGGCCCTCACATTTGGCCATTAAAGGATAATGGTGGCTGCTTGCCCCAGCTGC	2366
QY	1239	ACTGCACTGGCCATCACCAAGGAAAGATCCAAACAAACGCTTCCGGCCAGATACGGAAC	1298	Db	1749	ACGTGAAGGTTCCATATTAGGATTAAGGATAATGGCTTAAACTAGCTAAAGCTAAC	1690
Db	2829	CATCCAATGGTGTATTAACAAAGGATCCGGATACTGGTAAATGATTCACTGGGATACTGGAAC	2770	QY	2367	GGTAACCAAGCTGGTGTGCACTGGCAGCTGGCAATTGGCTGACGTGACAC	2426
QY	1359	C---GGTGGGAATACCGCTCACCAAGGAAACTTGTGCTTGAAGGCTCAGCT	1358	Db	1689	CGCTTACGAAATTGATTGAGTTACGGTAAATGGTTACCAATTCACTCTCACAC	1630
Db	2769	AATCATGGCTTATGGTCAAGGGGGCTTGGGTGTACTGCTGATGTTGAGATGGTT	2710	QY	2427	CCAGGACACTGGGGGGCCAGGCTGGCAACCCTACTTGTGCTGAGCTGGTGGCAGA	2486
QY	1416	TTCGCACTTGGAAACTGCTGGTCTGGCTGAGTTCAACGGTGTGTC	1475	Db	1569	TATCATGATACTGTTGCTTCAATGAGTGGTTAACAAACAGCAATTGCTGCTTC	1510
Db	2649	GATACTCATTTAACAAAGGAAAGAAAATGGTACGCTCATTACGAGAAATGGTATTTCG	2590	QY	2547	CATGTTGACGGTGCATTGGGCAACCGTGGGAGTACCTGGCTGAGCTGGCTTC	2546
QY	1476	TGGTGTGGCAACCAACATTGGTTCTGGCTGAGCTGGCTGAGCTTCAACTTC	1535	Db	1509	GTATATTATGGATTAACTGGTTCACTGGTAAACTGATATTGAAGGTATGGA	1450
Db	2589	TGGTGTAAAACATAATTCCATTCTAAATTAAATGTATAAGGATAAAAGTCAACAG	2530	QY	2607	TGACCTCGGGCTGACTGGAGGAGTGGCTGACTCTGGCATTTGAGTCTGGAAAC	2666
QY	1536	CAAGCGCATGCCACCGGATTCAATTGGCAACCCGACCTTCACCTGC	1595	Db	1449	GTCACCTAGTCATTATTGGTCAACTGTACTTATTTCAGACATTGGATGATGAA	1390
Db	2529	TGGTGTATTACACAACCTAAATTGAAAGAACCCGAACCTTCAACCTAGCCGT	2470	QY	2667	CCCAGGCCAACGGCTTACGCCACGAAATCCAGGGGACAGTTGTCCAAACCT	2726
QY	1596	TGATGTGAGCAGGGACCTCACTGGGATTACTTGGCAAGTGTACCGTGAAC-	1647	Db	1389	CAATCACCGAAATACTGTAATTATCAACATGAAATGGCTGGAGCTTGGAAATT	1330
Db	2469	TCTAGATAGAGGTACTAAACATTAGAATAATTAGGTTAATGTAACATTAGTGGT	2410	QY	2727	GGTGCACAGGCCACCGGACTTGGCTGGGATCGTTTCAAGGAAACTCACTGAA	2786
QY	1648	AAGGCCATGCTGCACTGCCACGGGTTCCCGTGAAGCAAGCTGGCTAACATC	1707	Db	1329	TCGCAGAGTGAATTGGTGAATTTGGTGAATGGTAAAGGATGATGAAAGTATGTA	1270
Db	2349	AAGTAATACTGGCTTCAATTAGGTTAGGGTACGAAACAACTTGTGTTGATGAA	2290	QY	2787	CGCAGGCCAACCTCGCACTCCCTGGTGGGCTGGGCTGGGGCGACCTGGCGGA	2906
QY	1767	GTTGCTGTGATCTCCGTGAGCAGGCGACTGGCAATTGGCTAACCTCCGGCA	1826	Db	1269	TGCTGATATGGTACAAAATGTACCTGGTCAAACTCGTCAAAAGTACAGA	1150
Db	2289	TGTAGCTGAATGGTTAAAAAGCAGGGATGATGGTACGAACTAACCTTAAAGA	2230	QY	2907	TCCACAAAAGTACGACATCCCAGACTCTGGTTCCTGGGGGGCGAGCTGGTAA	2966
QY	1827	TGCACACCAACTTGGCTGCGAACCCGAGTCGCTCAATTGGCAACTGAAAGC	1886	Db	1149	TGGCTATAATTAGATTCCAGAACATGCTGTTCAAAAGTGAATAGGACA	1090
Db	2229	TGCACACCAATCATATTAGCTACACGAGTTAGAACTAAGGATATGATTAA	2170				

PRIOR APPLICATION DATA:

APPLICATION NUMBER:	60/085,598
FILING DATE:	14 May 1998
APPLICATION NUMBER:	60/051571
FILING DATE:	JULY 2, 1997
ATTORNEY/AGENT INFORMATION:	
NAME:	Arielle, Pamela Deneke
REGISTRATION NUMBER:	40,489
REFERENCE/DOCKET NUMBER:	GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE:	(781) 893-5007
TELEFAX:	(781) 893-8277

INFORMATION FOR SEQ ID NO: 1156:

SEQUENCE CHARACTERISTICS:

LENGTH:	2922 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	double
TOPOLOGY:	circular
MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	NO
ANTI-SENSE:	NO
ORIGINAL SOURCE:	Enterococcus faecium

FEATURE:

NAME / KEY:	misc feature
LOCATION:	(B) LOCATION 1..:2922
SEQUENCE DESCRIPTION:	SEQ ID NO: 1156:

US-09-107-532A-1156

Query 2967 CCTCCAGGCTGGCCAGGCCACTGGCACCCGGCAACTGGAAAGGGCGTCCGAAGG 3026
 Database 1089 ACCTGTAAATGTTTAATAAGATTACAAGGGTTTAAAGGCAAGAACACT 1030

Query 3027 CAAGGCACCTCTGACGGAAAGCTCCGTGAGGAAGGCCCTCGACGCGTATGATT 3086
 Database 1029 AACAGCTCGTCCAGGTAAATCTAGGCCATTGATTGAGTTGAGTTGCT 970

Query 3087 CAAGGAACGTGCCAATAGCC-----TCAACCGCCTGCTGTTCCC 3125
 Database 969 TGAAGAAGGCAACAAGGTCTCTGTACGGAGCAAGATATTAGTTATGTAATATCC 910

Query 3126 GAAGCCAACCGAAGAGTTCTCGAGCACCGTGGCAAACACCTCTGGCTGGA 3185
 Database 909 AAAAGTATGAAACAATTATTCAAACTAGAAATCAAATACGAAAACATTATCGTTACTTGAA 850

Query 3186 TGATCGTGAATTCTTCTACGGCCCTGGTGAAGGGCGCGAGACTTGTATCCGCTGCCAGA 3245
 Database 849 TAGCCTACATTCTTCTGGAAATGCTGTAATG---GTTGAAACAGTGAATCGAAATCGA 793

Query 3246 TGTGGCACCCTACTGTTGGCTGGATCTCTGAGCCAGGATAAGGGTAT 3305
 Database 792 TAAAGGTAACGATTAAATTAAACTAGAAACGATTAGTGAACCATGAAATGGTAA 733

Query 3306 GCGCAATGTTGGCCAACGTCACGGCCAGATCCGCCAATGCTGTGGTACCGCTC 3365
 Database 732 TAGAACGATTACTATGGATGAAATGGTCAAGCGAGACGTATTACATTAAGATGAAAA 673

Query 3366 CGTGAGTCTGTCAACGGCAACCGAGATTCTCCAAACAGGGCCATGGTTC 3425
 Database 672 TGTGCATAAAATGGAACGTTAACGATAAGGTAATCCAAAGTCATATCGG 613

Query 3426 TGCACCATTCGCTGGTGTAC---CGTCACTGTTGGCTGAAGGTGATGAGGTCAAGGC 3482
 Database 612 TGCTCAAATGCCAGGTCAAGTAACCTGAAGTCAAGTTAGTGTGAAGACTGTGAAGGC 553

Query 3483 TGGAGATGAGTCGCAATCATCGAGGCTATGAAAGATGAAACAAATCACTGTTCTGT 3542
 Database 552 TAATCAGCCGTTGCTAAATTACTGAAGCTATGAAATGGAAACAACAAATTCAAGCACCATT 493

Query 3543 TGACGGCAAAATCGATCGGTTCCCTGTCGAACGAAGGTGGCAGACTT 3602
 Database 492 TGACGGTGTGATTAAACAGTAACCTGAAATGTTGACACAATGGGACAGGGATT 433

Query 3603 GATCGTCTGCGTT 3615
 Database 432 ATTAATCGAAATT 420

RESULT 9
 US-09-107-532A-1156
 Sequence 1156, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD/ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107, 532A
 ; FILING DATE: 30-Jun-1998

Query 616 CCAGTGTGGGAATCCACCCATCTTGTGAAGGGCACTCGTAAAGGCTGAA 675
 Database 421 TCGATTCAGGTCAGCTATGAGTCAAGGGGATGCT 420

Query 676 GGCCAGACTTACCCATCTTGTGAAGGGCACTCGTAAAGGCTGAA 735
 Database 481 CAATACGGTTATCCGATTATGATCAAGGGCAGCTATGCGGT 540

Query 736 TTGGTTGCTCACCTGATGAGCTTCGAACTAGAACAGAACATCTCGTAAAGGCTGAA 795
 Database 541 GTAGCTCACGATGAAAGAGGTGCAAGAGGCTACGAACGGAAACGGAAAA 600

Db 2755 AcTTTCTTCAGGAACTAGGGCAACCCGTTGGGGATTCCCTAAAAATTGCCAAAG 2814
 Qy 3001 CGGCCACTGGAAAGGCCCTCGAAGGCCAAGGCACCTC 3037
 Db 2815 ATTATTCCTAAAGGGAGACCTGCTTGAATGAACTGTC 2851

RESULT 10
 Sequence 1699, Application US/09543681A
 Patent No. 6605709
 GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 FILE REFERENCE: 2709-1002-001
 CURRENT APPLICATION NUMBER: US/09/543, 681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO 1699
 LENGTH: 1362
 TYPE: DNA
 ORGANISM: Proteus mirabilis
 US-09-543-681A-1699

Query Match 8.7%; Score 313.4; DB 4; Length 1362;
 Best Local Similarity 55.4%; Pred. No. 4.4e-79;
 Matches 721; Conservative 0; Mismatches 556; Indels 24; Gaps 5;

Qy 236 AAAAGATTTGGTAGCAAACCGGGGAATCGGGTCCGTGCTTCCGTGAGCACTCG 295
 Db 20 AAAAAATCCTCATTCGCAACCGTGGAAATTGCACTGGTATAAGAGCTTGTAAGG 79
 Qy 296 AAACCGGGTGCAGCCACGGTAGCTATTACCCCCGTAAAGATCGGGATCATTCCACCGCT 355
 Db 80 AACTTGGGATCAAAGGAGTCGGCGTTCACTCAGGGTAAATTAAACACGTTT 139
 Qy 356 CTTTTGCTCTGAAAGCTGTCGGCATTTGTAACCGTAAGGGTACCTGG 415
 Db 140 TGGCTGGCAGACGAGACTATCTGTATTGGTCCGCTGCTTCAGCA--AAAAGTTACTTAA 196
 Qy 416 ACATCGATGAAATTATGGTGGAGCTAAAGGAGATGGCATTACCGGGAT 475
 Db 197 ATATTCCGGCAATTATGGCCGAGAGATAAGTGGGGCAAGCCATTACCCAGGAT 256

Qy 476 ACGGCTTCTGTCTGAAATGCCAGCTGGGGAGGTGGTGGAAAACGGCAATTACTT 535
 Db 257 ATGGCTTCTGTCTGAAATGCCATTGGGAAACCAATTGGCTAACGGTTATT 316

Qy 536 TTATTGGCCAACCCAGGGTCTGGTCTGATCTCACCGGTATAAGTCTGGGGTAACCG 595
 Db 317 TTATTGGCTTAAGGGAAACCAATTGCCTAATGGGTGATAAAAGTTCCGCTATTGAAAG 376

Qy 596 CGGGAAAGGGCTGGTCTGGCAGTTGGTCTGATCTCACGGGTATAAGTCTGGGGTAACCG 649
 Db 377 GATGAAAAGGGGTGTCCTGTGTAACGGCTAGATGGCCATTAGGTAAACGATA 436

Qy 650 TCGATGAGATCGTTAAAAGGGCTGAAGCCAGACTTACCCATCTTGTGAAGGCAGTTG 709
 Db 437 CAGCCAAAATATCGAAATGCCAAACGCATGGTTACCTGTATTCAAGGCATCAG 496

Qy 710 CGGGTGGGGACGGGTATGGTTTGTGCTTCACTGATGAGCTTCGCAATTAG 769
 Db 497 GTGGTGGGGTGGTGGGTGAAGGTGAAGGGCTGGGTATGGTGTGTTGGCTCAAGGCA 556

Qy 770 CAAACAGAAGGCATCTGGTGAAGGTGAAGGGCTGGGTATATGTCGAAC 829
 Db 557 TCTCCATGACCCGTGGGAAGGCCAAAGGGGATTTAGAACGATATGGCTTATGGAA 616

Qy 830 GTGGCTGTGATTAACCCCTAGCATATTGAAACTGGCAGATCTGGGATCACGGAGAAG 889

Db 617 AGTACCTTGAATACTCCACGCCACGGTCAATTCAAGGTAAATG 676
 Qy 890 TTGTRACACCTTTATGAAACCGTGAACGTGCTCACTGCAACGGTGTGTCAGAA 949
 Db 677 CTATCTTATTAGTGTAAACGTGACTGCTCAATGCAACGTGTCAGAA 736
 Qy 950 TTGGGCCAGCACAGCAATTGGATCCAGAACTGGGTGATGCCGATGCAGTAA 1009
 Db 737 AAGCACAGCACGGTTACCCCTGAGATCCGTTAAATACTGGTGAACGCTGTGCAA 796
 Qy 1010 AGTCTGCGCTCCATTGGTTACCGGAACTGGTGTGATGAA 1069
 Db 797 ATGCCCTGTATTGAAATTGGCTACCGGGTACGTTGAAATTCTCTATGAA 853
 Qy 1070 AGGGAAACCACGTCATTGAAATGAACTCCAGGTTGAGCAACCGTGAACCTG 1129
 Db 854 ATGGGAAATTCTACTTTATCGAAATGAAATACCCGTTACCTGTACTG 913
 Qy 1130 AAGAAGTCACGGAGGTGGACCTGGTGAAGGGCAGATGGCCTGGCTGCAACCT 1189
 Db 914 AGATGATCACCGGTGTTGACCTTATCGAAAGGAAACTGCATCGCTTACCC-- 971
 Qy 1190 TGAAGGAATTGGCTGTGACCCAAAGATTAAGATCAAGAACCCACGGTGCAGTGCC 1249
 Db 972 -----ATTATCAGTCAGCAAGATCAAATTCACTGGACATGCTATTGAGTGCC 1024
 Qy 1250 GCATCACCACGGAAAGATCCAAACACGGCTTCGGCCAGATAACGGAAACTATCACCGCGT 1309
 Db 1025 GTATCAACGCAAGAGATCCAAA---CCCTCTTGCAGCCGGGAACCATCACTCGTT 1081
 Qy 1310 ACCGCTCACAGGGGGAGTTGGCTCTTGAAGGGTGCAGCTCGACTTGTGAA 1369
 Db 1082 TCCACTCACAGGGGATTGGTACGGTAACTTACGAGGTTACACCG 1141
 Qy 1370 TCACCGCACACTTGAECTCATGCTGGTGAATAATGACCTGCTGGTGGTTCGACTTGTGAA 1429
 Db 1142 TCCACCACTATGATTGATGTTACGGTAAATTGATCACTTACGGTAACTTACACCG 1201
 Qy 1430 CTGCTGTTGCTGGTGAACGGGGCTGGTGTGCTGGTGTGCAACCA 1489
 Db 1202 TGGCATTCTCGTATGAAAATGCTGGCAGAACTTATTGACGGCATTAAACCA 1261
 Qy 1490 ACATGGTTCTTGGTGGCTGGTGGCTGGGGAAAGGGACTTC 1530
 Db 1262 ATATGAGCTACACCAATTATTGAAATGATGAGCAATTTC 1302

RESULT 11
 US-07-956-700B-5
 ; Sequence 5, Application US/07956700B
 ; Patent No. 5539092
 GENERAL INFORMATION:
 APPLICANT: Robert Haselkorn and Piotr Gornicki
 TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
 TITLE OF INVENTION: Carboxylase
 NUMBER OF SEQUENCES: 116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5539092th Clark Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII-DO
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/956,700B
 FILING DATE: 1992/10/02
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:

NAME: Thomas E. NO. 5539092thrup
 REGISTRATION NUMBER: 33, 268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 1-312-744-0090
 TELEX: 1-312-755-489
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1362 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Oligonucleotide
 US-07-956-700B-5

Query Match 8.6%; Score 313; DB 1; Length 1362;
 Best Local Similarity 53.9%; Pred. No. 5.7e-79;
 Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;

```

Db 784 AAAGTCGCTCAAGGATCGGGCTACATCGGTGCCGGCACCGTGGAGTTCTGGTCAATGCGG 843
Qy 1069 AAGGGCAACCACTCGAAATGAACCGTATCCAGGTTGAGCACACCGTACTGACT 1128
Db 844 ACCGGCAACTCTACTTCATGGAGATAATCCGCATCCAAAGTCGAGCATCCAGTCACA 903
Qy 1129 GAAGAAGTCACCGAGGTGGACCTGGTAAGGGCGAGATGCGCTGGCTGGTCAACC 1188
Db 904 GAAATGATTACGGACTGGAATTCAGTTGGGAGGAGATTCGATTGCCAAGGG----- 958
Qy 1189 TTGAGGAAATTGGTCTGAGCCAAAGATAAGATAAGAACCCAGGGTGCAACTGCACTGC 1248
Db 959 ----AAGGGCTGGCTCCGGCAAGCGATATTCAACTGCGGGCATGCGATCGAATGCA 1014
Qy 1249 CGCATCACCACCGAAAGATCCAAGACCGTTCGGCCAGATAACCGGAACTATCACCGCG 1308
Db 1015 CGTATCAATGCGGAAGATCCGGAAATACAATTTCGGCCGAATCTGGCGCATTACAGGC 1074
Qy 1309 TACCGCTACCAAGGGGAGCTGGCTCGTCTGACGGTGOAGTCAGCTCGTGGCGCAA 1368
Db 1075 TATTACCGCCGGGGGATCCGGCTGATCGTGTGATCCCGACTACAGCAA 1134
Qy 1369 ATCACCGCACACTTGAATGCTGGTAAATGACCTGCCATGCTGGTCCGACTTTGAA 1428
Db 1135 ATTCCGCCTATTACGATTGCGTGTGATGGCAAATTGATTGTTGCAACACGGAA 1194
Qy 1429 ACTGCTGTTGCTGAGTTCACCGTGTCTGGTCAACCGTGTCTGGTGGTCAACC 1488
Db 1195 GAGGGCATCGGGATGCGGTCTGCGGAAATGGCCATCACCGGCTTGGGAGCG 1254
Qy 1489 AACATTGGTTCTTGGCGTGGCTGCGGGAAAGGAGACTTCACTTCAAGGGCATGCC 1548
Db 1255 ACCCTTAGTTCCATCAGTGTGATGTTGCAGATGGCTTCCGGGGAACTCTAT 1314
Qy 1549 ACCGGATTCAATG 1561
Db 1315 ACCAACATTGTTG 1327

```

RESULT 12
 US-08-476-537-5
 Sequence 5, Application US/08476537
 Patent No. 5756290

GENERAL INFORMATION:

- APPLICANT: Robert Haselkorn and Piotr Gornicki
- CORRESPONDENCE ADDRESS:
- STREET: 321 No. 5756290th Clark Street
- CITY: Chicago
- STATE: Illinois
- COUNTRY: USA
- ZIP: 60610
- COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy Disk
- COMPUTER: IBM PC Compatible
- OPERATING SYSTEM: PC-DOS/MS-DOS
- SOFTWARE: ASCII-DOS
- CURRENT APPLICATION DATA:
- APPLICATION NUMBER: US/08/476, 537
- FILING DATE:
- CLASSIFICATION: 435
- PRIOR APPLICATION DATA:
- APPLICATION NUMBER: 07/956, 700
- FILING DATE: 10/21/92
- ATTORNEY/AGENT INFORMATION:
- NAME: Thomas E. No. 5756290thrup
- REGISTRATION NUMBER: 33, 268
- REFERENCE/DOCKET NUMBER: ARCD: 058
- TELECOMMUNICATION INFORMATION:
- TELEPHONE: 1-312-744-0090

Page 20

TELEFAX: 1-312-755-4489
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11362 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Oligonucleotide
 JJS-08-476-537-5

Query Match	Start	End	Score	Similarity	Prey
	Best	Local		8.6%	
	Matches	Similarity		53.9%	
	718	Conservative	0	1	
QY	232	TTC	AAAGATCTTGGTAGCAA		
Db	7	TTC	AAAGATCTGATGCCAA		
QY	292	CTCGAAACCGGTGCAGCCACGGT			
Db	67	CAAGAACCTCGGATCGGCACGAT			
QY	352	CGCTCTTTGCTCTGAAGCTGT			
Db	127	GTGCAGTTAGCGGACCAAGCGGT			
QY	412	CTGGACATCGATAATTATCGGG			
Db	184	CTCAATATCCCACATCATGGC			
QY	472	GGATAACGGCTTCCTGTCTGAAAA			
Db	244	GGCTATGGCTTCGGGAGAAA			
QY	532	ACTTTTATTGGCCAACCCCCAGA			
Db	304	ACCTTTATTGGCCAGCCCCGA			
QY	589	GTAACCCGGAAAGAACGGCTGG			
Db	364	GAACAAATGGCAGGGTGGCGT			
QY	649	ATCGATGAGATCGTTAAAGGCC			
Db	424	GTTGATTGGCTGCCAAAGTTGG			
QY	709	GCCGGTGGGGGACGGGGTAT			
Db	484	GCGGGGGGGTGGTCGGGTAT			
QY	769	GCAACAGAAGGCATCTCGTGAAAGC			
Db	544	TTCCCTTGCTGCCAACGGAGAGC			
QY	829	CGTGTGTGATTAACCCCTCAGC			
Db	604	AAATTATCGATGCCAACGCC			
QY	889	GTTGTACACCTTATGAAACGTGA			
Db	664	GTAGTGCATCTAGGGAGGGGA			
QY	949	ATTGGCCCAGCACAGCATTGGGA			
Db	724	GAAGCCCCAGTCCATGGCTATC			
QY	1009	AGTTCTTGGCTCCATGGTAA			
Db	784	AAAGTGGCTCAAGGATCGGCTA			
QY	1069	AAGGGCAACCACGTCTTCAATCGA			
Db	844	ACCGGCAACTCTACTTCATGGG			

LT 13
8-485-607-5
Sequence 5, Application US/08485607
tent No. 5792627

GENERAL INFORMATION:

APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-COA
TITLE OF INVENTION: Carboxylase

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5792627th Clark Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60610

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. NO. 5792627thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058

TELECOMMUNICATION INFORMATION:

TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1362 base pairs
TYPE: Nucleic acid

STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Oligonucleotide
 US-08-485-607-5

Query	Match	Score	DB 1;	Length
Best	Local Similarity	8.6%	Score 313;	1362;
Matches	718;	Pred. NO. 5.7e-79;	Mismatches	600;
	Conservative	0;	Indels	15;
			Gaps	3;
Qy	232 TTCAAAAGATCTTGGTAGCAAACCGGGAAATCGGGTCCGTGCTTCCGTGCAGCA	291		
Db	7 TTCAACAGATCCTGATGCCATTGCGGAATTCTGGGCAACTTCCGTCTTG	66		
Qy	292 CTGAAACCGGGTGCAGCCACGGTAGCTTATTACCCCCGTGAAGATGGGGATCATTCAC	351		
Db	67 CAAGAACTCGGGATCGGCCATTGCGATCGCCGTTCACTGTGGATGCCAACGGCTCCAT	126		
Qy	352 CGCTCTTGTGAAAGCTTCTGAAGGCTTCCGCATTGGTACCCAGTCAAGGCTAC	411		
Db	127 GTGCAGTTAGGGAGAAGGGCTGTATGG---CGAAGGGCCAGGAAAGCTAT	183		
Qy	412 CTGGACATCGATGAAATTATCGGTGCAGCTAAAAAGTTAACCGATGCCATTACCCG	471		
Db	184 CTCATAATCCCCAACATCATGGGGGGCCTGACCCCTAATGCCAGGCCATTACCCC	243		
Qy	472 GGATAACGCCCTTCCTGTGAAATAATGCCAGTGTGCCGGAAGGTGCGGAAACGGCATT	531		
Db	244 GGCTATGCCCTCTGGGGAGAATGCCGGAATCTGGCCGATCACCATCTC	303		
Qy	532 ACTTTATGGCCAACCCCAAGAGTTCTGATCTACCGGTGATAAGTCTCGGC----G	588		
Db	304 ACCTTATGGCCCAAGCCCCATTGATTGAGTCGATGGGATTAATCCACCGCTAAG	363		
Qy	589 GTAACC GGCGAAGAAGGGTGGCTGCTGGCAGTTGGGAATCCACCCGGAAAC	648		
Db	364 GAAACAATGGCAGGGGTGGCTGGCTTCGAGGATTGGGCTGACGGTCTGTGACGGAT	423		
Qy	649 ATCGATGAGATCGTTAAAGGGCTGAAGGCAGACTAACCCATCTTTGTGAAGGCAGTT	708		
Db	424 GTTGATTGGCTGGCAAAGTTGGCTGGCTGAGGATCGGCTATCCGGTCAATGATAAGGGAAGC	483		
Qy	709 GCGGTTGGGGAGCGGGTATGGTTGGCTTACCTGTAGCTGAGCTTCGCAAAATTAA	768		
Db	484 GCGGGGGGGGGGGTGGTGGCTGGTGGCTGAGGCTGGCTGAGATCTGGAAAAGACTG	543		
Qy	769 GCAACAGAAGGCATCTCGTGAAGGTGAAGGGCTGAGCTTATGTGCGAA	828		
Db	544 TTCTTGTGCTGCCAACGGAGAAGCCGAGGCTGGCAGCTGGTAACTGGCAAT	603		
Qy	829 CGTGTGATTAACCTTATGAAACGTGACTGCTCACTGGAGCTTCTGGGATCACACTGGAGAA	888		
Db	604 AAATTATCGATGCCAACGCCAACGGAGAAGCCGAGCTGGTAACTGGCAAT	663		
Qy	889 GTTGTAACACCTTATGAAACGTGACTGCTCACTGGAGCTGCTCACCAAAGTTGTGAA	948		
Db	664 GTAGTGCATCTAGGGAGGGGATTGTCATTCAACGTCGTTGGAAATCCAGGACTGTATCTCGAA	723		
Qy	949 ATTGGCCAGCACGATTTGATCCAGACTGGTGAAGCTGCTGATGGCATTTGTCGAA	1008		
Db	724 GAAGCCCCAGTCGGCTATGGCAGACTGGGGCAAAATGGGGATGCGCGTC	783		
Qy	1009 AAGTTCTGGCTCAAGGATCGGCTACATGGTGGGGACCTGGGAAACCGTGGAA	1068		
Db	784 AAAGTGGCTCAAGGATCGGCTACATGGTGGGGACCTGGGAGTTCTGGTCA	843		
Qy	1069 AAGGGCAACCACTGCTTCAATGAAATGAACTCCACGATCCAGTTGAGCACACCGTGA	1128		
Db	844 ACCGGCAACTTCTACTTCATGGAGATGAATACCCGATCAAGTCGAGCATCAGTCACA	903		
Qy	1129 GAAGAAAGTCAACGGAGCTGGACCTGGTGAAGGGCAGATGGCTTGGTGTGCAACC	1188		
Db	904 GAAATGATTACGGGACTGGGACTTGTGATTGGGAGATTGGGATTGCCAAAGGG-----	958		

RESULT 14
 US-08-475-879-5
 Sequence 5, Application US/08475879
 Patent No. 5972644
 Patent No. 5972644 5786170
 GENERAL INFORMATION:
 APPLICANT: Robert Haselkorn and Piotr Gornicki
 TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
 TITLE OF INVENTION: Carboxylase
 NUMBER OF SEQUENCES: 116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: 321 No. 5972644 5786170th Clark Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60610
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII - DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475, 879
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: 536
 NAME: Thomas E. No. 5972644 5786170thrup
 REGISTRATION NUMBER: 33, 268
 REFERENCE/DOCKET NUMBER: ARCD:058
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 1-312-744-0090
 TELEFAX: 1-312-755-4489
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1362 base pairs
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Oligonucleotide
 US-08-475-879-5

Query Match 8.6%; Score 313; DB 2; Length 1362;
 Best Local Similarity 53.9%; Pred. No. 5.7e-79;
 Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;

Qy 232 TCAAAAGATCTGGTAGCAAACCGGGGAAATCGGGTCCGTGCTTCCGTGCAGCA 291
 Db 7 TCAACAAAGATCCTGATCGCCAATCGCCAAATCGCCACTTGT 66

Qy 292 CTGAAAACGGTCAAGCCACGGTAGCTATTACCCCCGTGAAGATGGGGATCATTCAC 351
 Db 67 CAAAGAACCTGGGATCGCACGATCGCGTTCACTCCACGTGGATCGCAACGGCTCCAT 126

Qy 352 CGCTCTTGTGCTTCTGAAGGTGTCGGCATTGGTACCGAAGGGCTCACCAAGGTAC 411
 Db 127 GTGCAGTTAGGGACGAAGGGCTGTATTGG---CGAAGGGCCAGCAGCAAAGCTAT 183

Qy 412 CTGGACATCGATGAAATTATCGGTGAGCTAAAGGAGATGCCATTACCCG 471
 Db 184 CTCATAATCCCCAACATCATGGGGGCCATTACCCCAATGCCAGGGCCATCACCCC 243

Qy 472 GATACGGGTTCTGTGCTGAAAATGCCAAGCTTGGCCGGAGTGTGGGGAAAAGGCATT 531
 Db 244 GGCTATGGTTCTGGGGAGAATGCCAAATCTGGCCGATCACCATCTC 303

Qy 532 ACTTTTATGGCCCAAACCCCAAAGGGTTCTGATCTCACGGTGTAAAGTCCTGGC---G 588
 Db 304 ACCTTTATGGCCCCAGCCCCGATTGATTGATTGAGTCCACCGCTAAG 363

Qy 589 GTAACCGCCGGAAGAACGGCTGTGGCTGCCAGGTTGGCGGAATCCACCGCTAAG 648
 Db 364 GAAACATGGAGGGTCCGGGTCCGGGTCCGGCAGATTCCGGCAGTGCAGGGAT 423

Qy 649 ATCGATGAGATCGTTAAAGCGCTGAAGGCCAGCTTACCCATCTTGTGAAGGCAGTT 708
 Db 424 GTTGATTGGCTGCCAAAGTGGCTGGCTGGCGAGATCGGCTATCCGCTCATGCAAGGACG 483

Qy 709 GCAACAGAAGGCTCTGGGACGGGTATGCTTGTGCTTCAACCTGATGAGCTTCCGAATTAA 768
 Db 484 GCGGGGGGGTGGCTGGCCACGGAGAACGGAGAACGGGACTGTATCTCGAA 603

Qy 769 GATGGCTGGGATGGCTGGCTGGGAGATGGGGTATATGTGCGAA 828
 Db 544 TTCCCTGGCTGCCAAAGGAGAACGGAGAACGGGAGCTTGGCTGGCTGGGCTGGATCTCGAA 543

Qy 829 CTCGCTGAGATAACCCCTGAGCATATTGAAAGTGCAGATCCCTGGGAGA 888
 Db 604 AAATTATCGATGCCAACGCCAGCTGCTGATTTCAAGTCTGGCCATGCCATGGCAAT 663

Qy 889 GTTGTACACCTTTATGAAACGTGACTCTGCTCACTGCAAGGGTGTGCGAA 948
 Db 664 GTAGTGCATCTAGGCCAGGGCATTTGGATCCAGAAACTTGGGTGCTCAACGGTGTGCGAA 723

Qy 949 ATTGGCCAGCACGGCATTTGGATCCAGAAACTTGGGTGATGCGATTGCGGATGCGAGTA 1008
 Db 724 GAAGGCCCAAGCTCAAGCGATGGCTATCGGGAGACCTGGGAAATGGGGATGCGCCGTC 783

Qy 1009 AAGTTCTGGCGCTCATGGATGGTACCGGGGGAAACCGTGGAAATTCTGGTGTGATGAA 1068
 Db 784 AAGGTGCTCAAGCGATGGCTATCGGGAGACCTGGGAACTGGGGATGCGATGGG 843

Qy 1069 AAGGGCAACCAACGTCATGAAATGAACTGGGAGCTTACCGGGTGGCAACC 1128
 Db 844 ACCGGCAACTTCTACTTCACTGGGATTAACCCGATCCAAGTGGGATCAGTCACA 903

Qy 1129 GAGAAGTACCGAGGTGGACCTGGTAAGGGCCAGATGGCTGGTGGCAACC 1188
 Db 904 GAATGATACGGGACTGGGAGATGGGAGATGCCAAAGGGG---- 958

Qy 1189 TTGAAGGAAATTGGGTCTGACCCAAAGATAAGATCAAGACCCACGGTGGGACTGGTGC 1248
 Db 959 ---AAGGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGGGCATGGAATATGC 1014

Qy 1249 CGCATCACCAGGAAAGATCCAACAAACGGCTTCGCCAGATACCGGAACTATCACCGCG 1308
 Db 1015 CGTATCAATGCGGAATACAATTCCGGCAATTACAGGG 1074

Qy 1309 TACCGCTCACCAAGGGAGCTGGCTAGCTGGTGGGAA 1368
 Db 1075 TATTACCGCCGGGCTGCTGATTCCTGTTAACCGACTAGCAA 1134

Qy 1369 ATCACGGCACACATTGACTCCATGGTGAAGAAATGACCTGGGGTGGTCCGACTTTGAA 1428
 Db 1135 ATTCCGCCTATTACGATTGCTGATGGCAAATGATTGTCRGGGTGCACACGGGAA 1194

Qy 1429 ACTGCTGTTGCTGTCGACGGCGGGTGGCTGAGTTCACCGTGTGTTGCAACC 1488
 Db 1195 GAGGGATGGGGATGAGGTGCTGGGAAATGCGCATCACGGGTTGCGGAGC 1254

Qy 1489 AACATTGGTTCTTGGTGTGGTTGCTGGGGAAAGGGACTTCACTTCCAAAGGGCATGCGC 1548
 Db 1255 ACCCTTAGTTCCATCAGCTGATGTTGAGATGCTGAGTTCTGCGGGAAACTCTAT 1314

Qy 1549 ACCGGATTCAATTG 1561
 Db 1315 ACCAACCTTGTG 1327

RESULT 15
 US-09-433-043B-5
 ; Sequence 5, Application US/09433043B
 ; Patent No. 6399342
 ; GENERAL INFORMATION:
 ; APPLICANT: HASIELKORN, ROBERT
 ; APPLICANT: GORNICKI, PIOTR
 ; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
 ; FILE REFERENCE: ARCD:338US
 ; CURRENT APPLICATION NUMBER: US/09/433 , 043B
 ; CURRENT FILING DATE: 1999-10-25
 ; PRIORITY FILING DATE: 1995-06-07
 ; PRIORITY APPLICATION NUMBER: 08/475, 879
 ; PRIORITY FILING DATE: 1992-10-02
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1362
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; US-09-433-043B-5
 Query Match 8.6%; Score 313; DB 4; Length 1362;
 Best Local Similarity 53.9%; Pred. No. 5.7e-79;
 Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;
 Matches 718; Conservative 0; Mismatches 600; Indels 15; Gaps 3;
 Qy 232 TACCGCTCACCAAGGGAGCTGGCTAGCTGGTGGGAAATCGGGTCCGTTCCGTGAGCA 291
 Db 724 GAAGGCCCAAGCTCAAGCGATGGCTATCGGGAGACCTGGGAAATGGGGATGCGCCGTC 783
 Qy 724 GAAGGCCCAAGCTCAAGCGATGGCTATCGGGAGACCTGGGAAATGGGGATGCGCCGTC 783
 Db 724 GAAGGCCCAAGCTCAAGCGATGGCTATCGGGAGACCTGGGAAATGGGGATGCGCCGTC 783
 Qy 1009 AAGTTCTGGCGCTCATGGATGGTACCGGGGGAAACCGTGGAAATTCTGGTGTGATGAA 1068
 Db 784 AAGGTGCTCAAGCGATGGCTATCGGGAGACCTGGGAACTGGGGATGCGATGGG 843
 Qy 1069 AAGGGCAACCAACGTCATGAAATGAACTGGGAGCTTACCGGGTGGCAACC 1128
 Db 844 ACCGGCAACTTCTACTTCACTGGGATTAACCCGATCCAAGTGGGATCAGTCACA 903
 Qy 1129 GAGAAGTACCGAGGTGGACCTGGTAAGGGCCAGATGGCTGGTGGCAACC 1188
 Db 904 GAATGATACGGGACTGGGAGATGGGAGATGCCAAAGGGG---- 958
 Qy 1189 TTGAAGGAAATTGGGTCTGACCCAAAGATAAGATCAAGACCCACGGTGGGACTGGTGC 1248
 Db 959 ---AAGGCTGCGCTTCCGGCAAGCCGATATTCAACTGCGGGCATGGAATATGC 1014
 Qy 1249 CGCATCACCAGGAAAGATCCAACAAACGGCTTCGCCAGATACCGGAACTATCACCGCG 1308
 Db 1015 CGTATCAATGCGGAATACAATTCCGGCAATTACAGGG 1074

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run-on: March 23, 2004, 20:24:42 ; Search time 1213 Seconds

(without alignments)
11042.568 Million cell updates/sec

Title: US-10-045-072-1

Sequence:
1 tggggcggggtttagatccctg.....tgatcgctgtttcccaa 3621

Perfect score: 3621

Scoring table: IDENTITY_NUC Gapop 10_0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 Summaries

Database :

```

1: /cgn2_6/podata/2/pubpna/us07_PUBCOMB.seq:*
2: /cgn2_6/podata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/podata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/podata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/podata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/podata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/podata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/podata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/podata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/podata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/podata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/podata/2/pubpna/US09_NNEW_PUB.seq:*
13: /cgn2_6/podata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/podata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/podata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/podata/2/pubpna/US10_NNEW_PUB.seq:*
17: /cgn2_6/podata/2/pubpna/us60_NEW_PUB.seq:*
18: /cgn2_6/podata/2/pubpna/us60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	100.0	3621	14	US-10-045-072-1
2	3621	100.0	3309400	9	US-09-738-626-1
3	3420	94.4	3420	9	US-09-738-626-765
4	3398.8	93.9	3474	9	US-09-974-973-1
5	3398.8	93.9	3474	9	US-09-974-973-3
6	1927.4	53.2	3423	12	US-10-282-122A-17701
7	1361.6	37.6	3381	12	US-10-282-122A-25766
8	1294.4	35.7	3384	12	US-10-282-122A-28626
9	1292.2	35.7	3381	12	US-10-282-122A-26500
10	681	18.8	3945	9	US-09-917-800A-1566
11	677.4	18.7	4017	9	US-09-880-107-3029
12	659	18.2	3432	15	US-10-369-493-31453
13	643.6	17.8	3459	15	US-10-369-493-35714
14	617	17.0	3441	15	US-10-369-493-35137
15	617	17.0	3453	15	US-10-369-493-38504

%

Result No.	Score	Query Match	Length	DB ID	Description
1	3621	100.0%	Score 3621;	DB 14;	Length 3621;
2	3621	100.0%	Pred. No. 0;	Mismatches 0;	Gaps 0;
3	3420	100.0%	Best Local Similarity 100.0%;	Conservative 0;	Matches 3621;
4	3398.8	100.0%	Query Match 100.0%;	Score 3621;	FILE REFERENCE: US-10-045-072-1
5	3398.8	100.0%	FILE REFERENCE: 1533.0790002	Length 3621;	CURRENT APPLICATION NUMBER: US-10-045-072-1
6	1927.4	100.0%	PRIOR APPLICATION NUMBER: US-09-677,575	Length 3621;	PRIOR FILING DATE: 2000-10-03
7	1361.6	100.0%	PRIOR APPLICATION NUMBER: US-09/220,081	Length 3621;	PRIOR FILING DATE: 2002-01-15
8	1294.4	100.0%	SEQ ID NO: 1	Length 3621;	PATENTIN Ver. 2.0
9	1292.2	100.0%	TYPE: DNA	Length 3621;	ORGANISM: Corynebacterium glutamicum
10	681	100.0%	FEATURE:	Length 3621;	
11	677.4	100.0%	NAME/KEY: CDS	Length 3621;	
12	659	100.0%	LOCATION: (199) .. (3621)	Length 3621;	
13	643.6	100.0%	US-10-045-072-1	Length 3621;	
14	617	100.0%	Qy 1 TGGGGGGGGTTAGATCCCTGGGGTTATTCACTTGAAACTGCTTGGCAGG 60	Length 3621;	
15	617	100.0%	Db 1 TGGGGGGGGTTAGATCCCTGGGGGGTTATTCACTTGAAAGTCGTGGCAGG 60	Length 3621;	

QY	121	AATCGGGGTTACGATACTAGGACCGAAGTGAATGCTATCACCCCTGGGGTCTCTGTG	180	QY	1201	GGTCGTGACCCAAAGATAAGATCAAGACCACGGTGAGCACTGAGTGCCTGCATCACCGACG	1260
Db	121	AATCGGGGTTACGATACTAGGACCGAAGTGAATGCTATCACCCCTGGGGTCTCTGTG	180	Db	1201	GGTCGTGACCCAAAGATAAGATCAAGACCACGGTGAGCACTGAGTGCCTGCATCACCGACG	1260
QY	181	AAAGGAATAATTACTCTAGTGTCCGACTCACACATCTTCAACGCTTCAGCATTCAAAG	240	QY	1261	GAAGATCCTAACAAACGGCTTCGGCCAGATACCGAAACTATCACCGGTAACCGCTCACCCA	1320
Db	181	AAAGGAATAATTACTCTAGGACCGAAGTGAATGCTATCACCCCTGGGGTCTCTGTG	240	Db	1261	GAAGATCCTAACAAACGGCTTCGGCCAGATACCGAAACTATCACCGGTAACCGCTCACCCA	1320
QY	241	ATCTGGTAGCAAACCGGGGAAATCGGGGAACTCGGTGCTCGTCAACGCTTCAGCATTCAAAG	300	QY	1321	GGCGGAGCTGGGTTGCGCTTGAAGTGCAGCTGGCAAGTCAAGCTGGTGGGAATCACCGCACAC	1380
Db	241	ATCTGGTAGCAAACCGGGGAAATCGGGGAACTCGGTGCTCGTCAACGCTTCAGCATTCAAAG	300	Db	1321	GGCGGAGCTGGGTTGCGCTTGAAGTGCAGCTGGCAAGTCAAGCTGGTGGGAATCACCGCACAC	1380
QY	301	GGTGCAGGCCACGGTAGCTATTACCCCCGGATCATCCACCGCTCTTT	360	QY	1381	TTTGACTCCATGCTGGTGAATAATGACCTGCGACTTGGAAACTGCTGTTGCT	1440
Db	301	GGTGCAGGCCACGGTAGCTATTACCCCCGGATCATCCACCGCTCTTT	360	Db	1381	TTTGACTCCATGCTGGTGAATAATGACCTGCGACTTGGAAACTGCTGTTGCT	1440
QY	361	GCTTCTGAAGCTGTCCGATTGGCTACCGTCAAGGCTAACCTGGACATC	420	QY	1441	CGTGCACAGCGGGGTTGGCTGAGTTAACCGTGTCTGGTGGAAACCAACATTGGTTTC	1500
Db	361	GCTTCTGAAGCTGTCCGATTGGCTACCGTCAAGGCTAACCTGGACATC	420	Db	1441	CGTGCACAGCGGGTTGGCTGAGTTAACCGTGTCTGGTGGAAACCAACATTGGTTTC	1500
QY	421	GATGAATTATCGGTGAGCTAAAGTAAAGCAGTGGCATTACCGGATAGGC	480	QY	1501	TTGCGTGCCTGCTGGCTGAGTTAACCGCATTGGCTACGGCATCGCCACGGATTCTATT	1560
Db	421	GATGAATTATCGGTGAGCTAAAGTAAAGCAGTGGCATTACCGGATAGGC	480	Db	1501	TTGCGTGCCTGCTGGCTGAGTTAACCGCATTGGCTACGGCATCGCCACGGATTCTATT	1560
QY	481	TTCCTGTCGAAATGCCAGGTTGAGCTAAAGTAAAGCAGTGGCATTACCGGATTATT	540	QY	1561	GCCGATCACCCGACCTCCAGGCTTACGGCTGCTGATGATGAGCAGGACGGCATCTG	1620
Db	481	TTCCTGTCGAAATGCCAGGTTGAGCTAAAGTAAAGCAGTGGCATTACCGGATTATT	540	Db	1561	GCCGATCACCCGACCTCCAGGCTTACGGCTGCTGATGATGAGCAGGACGGCATCTG	1620
QY	541	GCCCCAACCCCAGGGTCTGATCTCACCGTGTATAAGTCTCGGGTAACCGCCCG	600	QY	1621	GATTACTTGGCAGATGTCACCGTGTCAAGGCTTACGGCTTACGGCTTACGGCT	1680
Db	541	GCCCCAACCCCAGGGTCTGATCTCACCGTGTATAAGTCTCGGGTAACCGCCCG	600	Db	1621	GATTACTTGGCAGATGTCACCGTGTCAAGGCTTACGGCTTACGGCTTACGGCT	1680
QY	601	AGAAGGGTGGTCTGCAAGTTGGGGAACTACCCCATCTGGGAAATCCACGGAA	660	QY	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATCTGGCAGTCTGGCAGTCCGC	1740
Db	601	AGAAGGGTGGTCTGCAAGTTGGGGAAATCCACGGAA	660	Db	1681	GCTCTATCGATAAGCTGCTAACATCAAGGATCTGGCAGTCTGGCAGTCCGC	1740
QY	661	GTAAAGGGCTGAAGCCAGACTTACCCCATCTGGGAAATCCACGGAA	720	QY	1741	CGCTGAAGCAGCTGGCCAGGCCAGGGCGTTGGCTGAGCAGGACGCACTG	1800
Db	661	GTAAAGGGCTGAAGCCAGACTTACCCCATCTGGGAAATCCACGGAA	720	Db	1741	CGCTGAAGCAGCTGGCCAGGCCAGGGCGTTGGCTGAGCAGGACGCACTG	1800
QY	721	GAACGGGGTATGCTTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	780	QY	1801	GCAGTTACTGATACACACCGATCTGGGATGACCTTGGGAGCCGGAGTCCGC	1860
Db	721	GAACGGGGTATGCTTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	780	Db	1801	GCAGTTACTGATACACACCGATCTGGGATGACCTTGGGAGCCGGAGTCCGC	1860
QY	781	TCTCGTGAAGCTGAAGGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	840	QY	1861	TCATTCGGCACTGAGCCGGCTGGGGAGGGCTGGCTGGCTGGCTGGCT	1920
Db	781	TCTCGTGAAGCTGAAGGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	840	Db	1861	TCATTCGGCACTGAGCCGGCTGGGGAGGGCTGGCTGGCTGGCTGGCT	1920
QY	841	AACCCCTGAGCATATTGAGTGGCAGATCCTTGGGATCACACTGGAGAAGTTGTACACCTT	900	QY	1921	GTGGAGGCCTGGGGGGGGGACCTAGATGGGGGATGGCTTGGGGATGGCTTGGGG	1980
Db	841	AACCCCTGAGCATATTGAGTGGCAGATCCTTGGGATCACACTGGAGAAGTTGTACACCTT	900	Db	1921	GTGGAGGCCTGGGGGGGGGACCTAGATGGGGGATGGCTTGGGGATGGCTTGGGG	1980
QY	901	TATGAAAGGTGACTGCTCACTGGAGCTGGTCAACCAAAAAGTTGGCCAGCA	960	QY	1981	TGGGACAGGGCTGACGGAGCTGGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2040
Db	901	TATGAAAGGTGACTGCTCACTGGAGCTGGTCAACCAAAAAGTTGGCCAGCA	960	Db	1981	TGGGACAGGGCTGACGGAGCTGGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2040
QY	961	CAGCATTGGATCCAGAACCTGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	1020	QY	2041	CGGGCCGAAACACCGTGGCTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2100
Db	961	CAGCATTGGATCCAGAACCTGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	1020	Db	2041	CGGGCCGAAACACCGTGGCTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2100
QY	1021	TCCATTGGTTACCAAGCCACGATTCAGGTTGGGGATGGCTTGGGGATGGCTTGGGG	1080	QY	2101	AAGGAAGGTGGCTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2160
Db	1021	TCCATTGGTTACCAAGCCACGATTCAGGTTGGGGATGGCTTGGGGATGGCTTGGGG	1080	Db	2101	AAGGAAGGTGGCTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2160
QY	1081	GCTCTCATGAAATGAACCCACGATTCAGGTTGGGGATGGCTTGGGGATGGCTTGGGG	1140	QY	2221	GCTATGGCTTATTCCTGGTGAATTCCTGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2280
Db	1081	GCTCTCATGAAATGAACCCACGATTCAGGTTGGGGATGGCTTGGGGATGGCTTGGGG	1140	Db	2221	GCTATGGCTTATTCCTGGTGAATTCCTGGGATGGCTTGGGGATGGCTTGGGGATGGCTTGGGG	2280
QY	1141	GAGGTGGACCTGGGCAAGGGGGAGGGAGATGGCTGGGGCAACCTTGAAGGAATTG	1200	QY	2281	TACCTAAAGATGGGAGGGAGATGGCTGGGGCAACCTTGAAGGAATTG	2340
Db	1141	GAGGTGGACCTGGGCAAGGGGGAGGGAGATGGCTGGGGCAACCTTGAAGGAATTG	1200	Db	2281	TACCTAAAGATGGGAGGGAGATGGCTGGGGCAACCTTGAAGGAATTG	2340

2281 TACCTAAAGATGGCAGGGAGATGGTCAAGTCTGGCTCACATCTGGCATTAAGGAT 2340
 Db 3361 CGTCCTGGTGAAGTCGTCACCGCAAACCGCAGAAAAGGCAGATTCTCCAACAAGGCCAT 3420
 Qy 3421 GTTGCTGCCATTGCTGTTGACTGCTGGTCAACGGTCAAGTGGTGAAGGTGATGAGGTCAAG 3480
 Db 3421 GTTGCTGCCATTGCTGTTGACTGCTGGTCAACGGTCAAGTGGTGAAGGTGATGAGGTCAAG 3480
 2341 ATGGCTGGCTGCTGGCTGGTAAACCAGGTGGTACCGTGGTCACTGGCAGCTGGTCAA 2400
 Qy 3481 GCTGAGATGGCAGTCGAATCATCGAGGCTATGAAGATGGAACAAATCACTGCTTCT 3540
 Db 3481 GCTGAGATGGCAGTCGAATCATCGAGGCTATGAAGATGGAACAAATCACTGCTTCT 3540
 2401 TTCGATCTGCCAGTGCAGTGCAACCCACGAAACTGGGGTGGCCAGGTGGCAACCTAC 2460
 Db 3541 GTTACGGCAAATCGATCGGTTGCTGGTCTGCAACGAAAGGTGAAAGGTGGCGAC 3600
 Qy 3541 GTTACGGCAAATCGATCGGTTGCTGGTCTGCAACGAAAGGTGAAAGGTGGCGAC 3600
 Db 3541 GTTACGGCAAATCGATCGGTTGCTGGTCTGCAACGAAAGGTGGCGAC 3600
 2401 TTCGATCTGCCAGTGCAGTGCAACCCACGAAACTGGGGTGGCCAGGTGGCAACCTAC 2460
 Db 3601 TTGATCGTCGTTCTAA 3621
 Qy 3601 TTGATCGTCGTTCTAA 3621
 Db 3601 TTGATCGTCGTTCTAA 3621

RESULT 2
 US-09-738-626-1
 / Sequence 1, Application US/09738626
 / Publication No. US20020197605A1
 / GENERAL INFORMATION:
 / APPLICANT: NAKAGAWA, SATOSHI
 / APPLICANT: MIZOGUCHI, HIROSHI
 / APPLICANT: ANDO, SEIKO
 / APPLICANT: HAYASHI, MIKIRO
 / APPLICANT: OCHIAI, KEIKO
 / APPLICANT: YOKOI, HARUHIKO
 / APPLICANT: TATEISHI, NAOKO
 / APPLICANT: SENOH, AKIHIRO
 / APPLICANT: IKEDA, MASATO
 / APPLICANT: OZAKI, AKIO
 / TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 / FILE REFERENCE: 249-125
 / CURRENT APPLICATION NUMBER: US/09/738,626
 / CURRENT FILING DATE: 2000-12-18
 / PRIOR APPLICATION NUMBER: JP 99/377484
 / PRIOR FILING DATE: 1999-12-16
 / PRIOR APPLICATION NUMBER: JP 00/159162
 / PRIOR FILING DATE: 2000-04-07
 / PRIOR FILING DATE: 2000-08-03
 / NUMBER OF SEQ ID NOS: 7059
 / SOFTWARE: PatentIn ver. 3.0
 / SEQ ID NO 1
 / LENGTH: 3309400
 / TYPE: DNA
 / ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1

Query Match 100.0%; Score 3621; DB 9; Length 3309400;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGGGGGGTTAGATCCTGGGGTTATTTOATTCACTTGGCTTGAAGTGTGTCAGG 60
 Db 705013 TGGGGGGGGTTAGATCCTGGGGGGTTATTTOATTCACTTGGCTTGAAGTGTGTCAGG 705072
 2581 ACCACCTCCAGCCATCCCTGTCGCATTGTCGATGCTGGCATTGGCTGC 2580
 Qy 2641 CTGTAACCTGCCATTGCTGAGTCGGTCACTGGCCACGAACTGGGAT 2700
 Db 2641 CTGTAACCTGCCATTGCTGAGTCGGTCACTGGCCACGAACTGGGAT 2700
 2641 ATCCCAGGGGACAGTTGCCAACCTGGGACACTGGCACGGCACTGGGAT 2760
 Qy 2701 ATCCCAGGGGACAGTTGCCAACCTGGGACACTGGCACGGCACTGGGAT 2760
 Db 2701 ATCCCAGGGGACAGTTGCCAACCTGGGACACTGGCACGGCACTGGGAT 2760
 2761 CGTTTCGAACCTCATCGAAGACAACTAACGGGCGTTAATGAGATGCTGGGACGCCAAC 2820
 Qy 2761 CGTTTCGAACCTCATCGAAGACAACTAACGGGCGTTAATGAGATGCTGGGACGCCAAC 2820
 Db 2821 AAGGTCAACCCATCCCTCAAGGTGCTGGGACCTCCACCTCGCACTCGCACTCGGACTCTGGGAC 2880
 Qy 2821 GTGGATCAGGAGACTTGTGGGACATCCAGACTCTGGGAC 2880
 Db 2821 AAGGTCAACCCATCCCTCAAGGTGCTGGGACCTCTGGGAC 2880
 2881 GTGGATCAGGAGACTTGTGGGACATCCAGACTCTGGGAC 2940
 Qy 2881 GTGGATCAGGAGACTTGTGGGACATCCAGACTCTGGGAC 2940
 Db 2881 GTGGATCAGGAGACTTGTGGGACATCCAGACTCTGGGAC 2940
 2941 GCGTTCTGGGGGGAGCTTGGTAACCCCTCAGGTGGCCAGAGCCACTGGGACCC 3000
 Qy 2941 GCGTTCTGGGGGGAGCTTGGTAACCCCTCAGGTGGCCAGAGCCACTGGGACCC 3000
 Db 2941 GCGTTCTGGGGGGAGCTTGGTAACCCCTCAGGTGGCCAGAGCCACTGGGACCC 3000
 3001 CGCGCACTGGAAGGCAAGGCCAACCTTGACGGAAAGTTCTGGGAAAGAG 3060
 Qy 3001 CGCGCACTGGAAGGCAAGGCCAACCTTGACGGAAAGTTCTGGGAAAGAG 3060
 Db 3001 CGCGCACTGGAAGGCAAGGCCAACCTTGACGGAAAGTTCTGGGAAAGAG 3060
 3061 CAGGGCAACCTGACGCTGATGATTCCAAGGAACGTCGCTCAACGCCCTGCTG 3120
 Qy 3061 CAGGGCAACCTGACGCTGATGATTCCAAGGAACGTCGCTCAACGCCCTGCTG 3120
 Db 3121 TTCCGAAAGCCAACCGAAGACTCTCGAGCACCCGCTTGGCAACACCTCTGCG 3180
 Qy 3121 TTCCGAAAGCCAACCGAAGACTCTCGAGCACCCGCTTGGCAACACCTCTGCG 3180
 3121 TTCCGAAAGCCAACCGAAGACTCTCGAGCACCCGCTTGGCAACACCTCTGCG 3180
 3181 CTGGATGATCGTCGACCCACTGCTGGCAAGGCGAGACTTGTGCTGGCTGCG 3240
 Qy 3181 CTGGATGATCGTCGACCCACTGCTGGCAAGGCGAGACTTGTGCTGGCTGCG 3240
 Db 3241 CCAGATGTCGGCAACCCACTGCTGGCAAGGCGAGACTTGTGCTGGCTGCG 3240
 Qy 3241 CCAGATGTCGGCAACCCACTGCTGGCAAGGCGAGACTTGTGCTGGCTGCG 3240
 Db 3301 GGTATGCCAATGTTGCTGCCAACGCCAGATCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3360
 Qy 3301 GGTATGCCAATGTTGCTGCCAACGCCAGATCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3360
 Db 3301 GGTATGCCAATGTTGCTGCCAACGCCAGATCGCTGGATGCGATCTCTGAGCCAGACGATAAG 3360
 Qy 3361 CGCTCCGTTGAGTCTGTCACCGCAACGGCAAGATTCCCTCAACAGGCCAT 3420
 Db 3421 CGCTCCGTTGAGTCTGTCACCGCAACGGCAAGATTCCCTCAACAGGCCAT 3420
 Qy 3421 CGCTCCGTTGAGTCTGTCACCGCAACGGCAAGATTCCCTCAACAGGCCAT 3420

	705253	ATCTTGGTAGCAAACCGGGCAAATCGGGTCCGTCGAGCAACTCGAACC	705312	
301	GTTGCCAACGGTAGCTATTACCCCCGTGAAGATCGGGATCATTCACCGGCTCTTT	360		
705313	GTTGCCAACGGTAGCTATTACCCCCGTGAAGATCGGGATCATTCACCGGCTCTTT	705372		
361	GCTTCTGAAGCTGTCGGCATTGGTACCGAAGGTCAAGGGTACCTGGACATC	420		
705373	GCTTCTGAAGCTGTCGGCATTGGTACCGAAGGTCAAGGGTACCTGGACATC	705432		
421	GATGAATTATCGTGCAGCTAAAGCAGATGCCATTACCGGGATACGGC	480		
705433	GATGAATTATCGTGCAGCTAAAGCAGATGCCATTACCGGGATACGGC	705492		
481	TTCCTGTAAGAAATGCCAGCTTGCCGGAGTGTGCCGAAAACGGCATTACTTTATT	540		
705493	TTCCTGTAAGAAATGCCAGCTTGCCGGAGTGTGCCGAAAACGGCATTACTTTATT	705552		
541	GGCCCAACCCAGAGGTTCTGATCTCACCGGTGATAAGTCTCGCCGGTAAACCGCCGG	600		
705553	GGCCCAACCCAGAGGTTCTGATCTCACCGGTGATAAGTCTCGCCGGTAAACCGCCGG	705612		
601	AAGAACGGCTGGCTGGCTGGGGAAATCACAACGGGAGAGTC	660		
705613	AAGAACGGCTGGCTGGCTGGGGAAATCACAACGGGAGAGTC	705672		
661	GTAAAGGGCTGAAAGGGCAAGACTAACCCATCTTGTGAAGGCAGTTGCCGGTGGC	720		
705673	GTAAAGGGCTGAAAGGGCAAGACTAACCCATCTTGTGAAGGCAGTTGCCGGTGGC	705732		
721	GGACGGCGTATGCGTTTGTGCTCACCTGAGCTTGGCAAAATTAGCAACAGAACGA	780		
705733	GGACGGCGTATGCGTTTGTGCTCACCTGAGCTTGGCAAAATTAGCAACAGAACGA	705792		
781	TCTCGTGAAGCTGAAGGGCTTCGGCGATGGCGGTATATGTCGAACGTGCTGTGATT	840		
705793	TCTCGTGAAGCTGAAGGGCTTCGGCGATGGCGGTATATGTCGAACGTGCTGTGATT	705852		
841	AACCTCTAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGACACCTT	900		
705853	AACCTCTAGCATATTGAAGTGCAGATCCTTGGCGATCACACTGGAGAAGTTGACACCTT	705912		
901	TATGAACGTGACTGCTCACTGCAAGGGCGTCAACGGTGGGATTAAGTTGGCAATTGGCCAGCA	960		
705913	TATGAACGTGACTGCTCACTGCAAGGGCGTCAACGGTGGGATTAAGTTGGCAATTGGCCAGCA	705972		
961	CAGCATTTGGATCCGAACACTGGCTGATGGCATTGTGCGGGATGGCGATTCTGGCC	1020		
705973	CAGCATTTGGATCCGAACACTGGCTGATGGCATTGTGCGGGATGGCGATTCTGGCC	706032		
1021	TCCATTGGTACCAAGGGCGGGAAACCGTGGGATTCTGGCTGATGAAAGGGCAACCA	1080		
706033	TCCATTGGTACCAAGGGCGGGAAACCGTGGGATTCTGGCTGATGAAAGGGCAACCA	706092		
1081	GTCTTCATCGAACATGAACCCACCGTATCCAGGTGACTGAAGAAGTCACC	1140		
706093	GTCTTCATCGAACATGAACCCACCGTATCCAGGTGACTGAAGAAGTCACC	706152		
1141	GAGGTGACCCAAGATAAGATCAAGAACCCACGGCAGATGGCCTGGCAACCTTGAAGGAATG	1200		
706153	GAGGTGACCCAAGATAAGATCAAGAACCCACGGCAGATGGCCTGGCAACCTTGAAGGAATG	706212		
1201	GGTCTGACCCAAGATAAGATCAAGAACCCACGGCAGATGGCCTGGCAACCTTGAAGGAATG	1260		
706213	GGTCTGACCCAAGATAAGATCAAGAACCCACGGCAGATGGCCTGGCAACCTTGAAGGAATG	706332		
1261	GAAGATCCAACAAACGGCTTCCGCCAGATAACGGAAACTATACCGCGTACCGCTCACCA	1320		
706293	TAACCTAAAGATGGCAGGGAGATCGTCAAGTCTGGCTCACATCTTGGCCATTAAAGGAT	707352		
2341	ATGGCTGGTCTGCCAGTGTGACACCCACGGACACTGGGGTGGCCAGCTGGCAACCTAC	2400		
707353	ATGGCTGGTCTGCCAGTGTGACACCCACGGACACTGGGGTGGCCAGCTGGCAACCTAC	2460		
2401	TTGATCTGCCAGTGTGACACCCACGGACACTGGGGTGGCCAGCTGGCAACCTAC	707472		
707413	TTGGATCTGCCAGTGTGACACCCACGGACACTGGGGTGGCCAGCTGGCAACCTAC	707472		

QY 2461 TTGCTGAAGCTCAAGCTGGAGATGCTGTGACGGTTCGGCACCCTGCTGGC 2520 QY 3541 GTTGACGGCAAATAATCGATGCCATTGGTTCCCTGCTGAAACGAAAGGTGGCGAC 3 600
Db 707473 TTGCTGAAGCTCAAGCTGGAGATGCTGTGACGGTTCGGCACCCTGCTGGC 707532 Db 708553 GRTGACGGCAAATAATCGATGCCATTGGTTCCCTGCTGAAAGGTGGCGAC 708612

QY 2521 ACCACCTCCAGCCATTCCCTGTCGCCATTGGCTGACCGTGGCGAT 2580 QY 3601 TTGATCGTCGTCGTTCCCAA 3 621
Db 707533 ACCACCTCCAGCCATTCCCTGTCGCCATTGGCTGACCGTGGCGAT 707592 Db 708613 TTGATCGTCGTCGTTCCCAA 708633

QY 2581 ACCGGTTTGAGGCTCGAGGCTGTTCTGACTCTGAGCTCGAGCCGTAAGCAGTGGCA 2640
Db 707593 ACCGGTTAGGCCATTGGCTCGAGCTGTTCTGACTCTGAGCCGTAAGCAGTGGCA 707652
QY 2641 CTGTAACCTGCCATTGAGTCTGGAAACCCCAACGGGTCGCTAACGCCAACGAA 2700
Db 707653 CTGTAACCTGCCATTGAGTCTGGCTAACGCCAACGAA 707712
QY 2701 ATCCCAAGGGACAGTGTCCAAACCTGCGTGCACAGGCCAACGGCACTGGGCGAT 2760
Db 707713 ATCCCAAGGGACAGTGTCCAAACCTGCGTGCACAGGCCAACGGCACTGGGCGAT 707772
QY 2761 CGTTTCGAACCTCATCGAAGACAACCTACGCAAGCCGTTATGAGATGCTGGCA 2820
Db 707773 CGTTTCGAACCTCATCGAAGACAACCTACGCAAGCCGTTATGAGATGCTGGCA 707832
QY 2821 AAGGTCAACCCCCATCTCCAAAGCTGGCTGGCACCTCCACCTCTGTCTGCATC 2880
Db 707833 AAGGTCAACCCCCATCTCCAAAGCTGGCTGGCACCTCTGTCTGCATC 707892
QY 2881 GTGGATCCAGGAGACTTTGGCTGGCACCTCCAAAGCTGGCTGGCACCTCTGTCTGCATC 2940
Db 707893 GTGGATCCAGGAGACTTTGGCTGGCGATCCAAAGCTGGCTGGCACCTCTGTCTGCATC 707952
QY 2941 GCGTTCCTGGCGGAGCTTGGTAACCTTCCAGGTGGCTGGCACCTCTGTCTGCATC 3 000
Db 707953 GCGTTCCTGGCGGAGCTTGGTAACCTTCCAGGTGGCTGGCACCTCTGTCTGCATC 708012
QY 3 001 CGCGCACTTGGAAAGGCCACCTCTGTGACGGAAAGTTCCCTGAGGAAGAG 3 060
Db 708013 CGCGCACTTGGAAAGGCCACCTCTGTGACGGAAAGTTCCCTGAGGAAGAG 708072
QY 3 061 CAGGGCACCTCTGAGCTGATGATTCCAAGGAACGTCCTCAACCGCTGCTG 3 120
Db 708073 CAGGGCACCTCTGAGCTGATGATTCCAAGGAACGTCCTCAACCGCTGCTG 708132
QY 3 121 TTCCCGAAAGCCAAACGCCAAAGGAAAGAGTCTCTGAGCACCCGTTGGCAACACCTCTGCG 3 180
Db 708133 TTCCCGAAAGCCAAACGCCAAAGGAAAGAGTCTCTGAGCACCCGTTGGCAACACCTCTGCG 708192
QY 3 181 CTGGATCGTGAATTCTTCAGGGCTGGATGGCAAGGCCAGAGACTTGTGTCGGCTG 3 240
Db 708193 CTGGATCGTGAATTCTTCAGGGCTGGATGGCAAGGCCAGAGACTTGTGTCGGCTG 708252
QY 3 241 CCAGATGTCGCAACCCCAACTGTTGTTGGCCAAAGTCAAGGGCCAGGAAATGGCTGGGATCTCTGAGGATAAG 3 300
Db 708253 CCAGATGTCGCAACCCCAACTGTTGTTGGCCAAAGTCAAGGGCCAGGAAATGGCTGGGATCTCTGAGGATAAG 708312
QY 3 301 GGATATGCCAAATGGTGGCCAAAGTCAAGGGCCAGTCCGGCAATGGCTGGTGAC 3 360
Db 708313 GGATATGCCAAATGGTGGCCAAAGTCAAGGGCCAGTCCGGCAATGGCTGGTGAC 708372
QY 3 361 CGTCCTGGCACCATGGCTGTCAACGCCAAAGGAGATTCCAAACAGGGCCAT 3 420
Db 708373 CGTCCTGGCACCATGGCTGTCAACGCCAAAGGAGATTCCAAACAGGGCCAT 708432
QY 3421 GTTGCTGACCAATTGGCTGGTGTGACCTGTTGCTGAAAGGTGATGAGGTCAAG 3 480
Db 708433 GTTGCTGACCAATTGGCTGGTGTGACCTGTTGCTGAAAGGTGATGAGGTCAAG 708492
QY 3481 GCTGGAGATGCACTGGCAATTGCAATCGAGGCTATGAAGATGGAAGGCAAAATCAGTCGTTCT 3 540
Db 708493 GCTGGAGATGCACTGGCAATTGCAATCGAGGCTATGAAGATGGAAGGCAAAATCAGTCGTTCT 708552
QY 3549 GTTGATCTCACCCGGTGTAAAGTCTCGCGGGTAAACCGCCGGTGTGGCTGGCGAC 6 18
Db 301 GAGCTTGGCGGAGTGTGGCAACCCAGAGTTTTGGCCAAACCCAGAGTT 3 60
QY 3559 CTTGATCTCACCCGGTGTAAAGTCTCGCGGGTAAACCGCCGGTGTGGCTGGCGAC 6 18
Db 361 CTTGATCTCACCCGGTGTAAAGTCTCGCGGGTAAACCGCCGGTGTGGCTGGCGAC 4 20

QY 3641 GTTGACGGCAAATAATCGATGCCATTGGTTCCCTGCTGAAACGAAAGGTGGCGAC 3 600
Db 708553 GRTGACGGCAAATAATCGATGCCATTGGTTCCCTGCTGAAAGGTGGCGAC 708612
QY 3601 TTGATCGTCGTCGTTCCCAA 3 621
Db 708613 TTGATCGTCGTCGTTCCCAA 708633
QY 3 621 Sequence 765, Application US/09738626
Db 708633 Publication No. US20020197605A1
QY 3 621 General Information:
Db 708633 Applicant: NAKAGAWA, SATOSHI
QY 3 621 Applicant: MIZOGUCHI, HIROSHI
Db 708633 Applicant: ANDO, SEIKO
QY 3 621 Applicant: HAYASHI, MIKI
Db 708633 Applicant: OCHIAI, KEIKO
QY 3 621 Applicant: YOKOI, HARUHIKO
Db 708633 Applicant: TATEISHI, NAOKO
QY 3 621 Applicant: SENOH, AKIHIRO
Db 708633 Applicant: IKEDA, MASATO
QY 3 621 Applicant: OZAKI, AKIO
QY 3 621 Title of Invention: NOVEL POLYNUCLEOTIDES
Db 708633 File Reference: 249-125
QY 3 621 Current Application Number: US/09/738, 626
Db 708633 Current Filing Date: 2000-12-18
QY 3 621 Prior Application Number: JP 99/377484
Db 708633 Prior Filing Date: 1999-12-16
QY 3 621 Prior Application Number: JP 00/159162
Db 708633 Prior Filing Date: 2000-04-07
QY 3 621 Prior Application Number: JP 00/280988
Db 708633 Prior Filing Date: 2000-08-03
QY 3 621 Number of SEQ ID Nos: 7059
Db 708633 Software: PatentIn ver. 3.0
QY 3 621 SEQ ID NO 765
Db 708633 LENGTH: 3420
QY 3 621 TYPE: DNA
Db 708633 ORGANISM: Corynebacterium glutamicum
QY 3 621 US-09-738-626-765

QY 3 621 Query Match 94.4%; Score 3420; DB 9; Length 3420;
Db 708633 Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
QY 3 621 Matches 3420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GTGTCGACTCACACATCTCAACGCTTCCAGCATTTCAAAAGATCTTCGCTAGCAAACCGC 258
Db 1 GTGTCGACTCACACATCTCAACGCTTCCAGCATTCAAAAGATCTTCGCTAGCAAACCGC 60

QY 259 GCGAAATCGGGTCGGTCTGGCTGGCAACGCCACCTCGAACTCGAACGGTAGCT 3 18
Db 61 GCGAAATCGGGTCGGTCTGGCTGGCAACGCCACCTCGAACTCGAACGGTAGCT 120

QY 319 ATTACCCCCGTGAAGATGGGGATCATTCACCGCTCTTCTGCTTCTGAAGCTGTCGGC 3 78
Db 121 ATTACCCCCGTGAAGATGGGGATCATTCACCGCTCTTCTGCTTCTGAAGCTGTCGGC 190

QY 379 ATTGGTACCGAAGGCTACCCAGTCAAGGGTACTCTGGACATCGATGAATTATCGTGTGCA 4 38
Db 181 ATTGGTACCGAAGGCTACCCAGTCAAGGGTACTCTGGACATCGATGAATTATCGTGTGCA 240

QY 439 GCTAAAAAGTTAACGCAATGGCTTACGGCTTCCTGCTGCTGAAATGCG 4 98
Db 241 GCTAAAAAGTTAACGCAATGGCTTACGGCTTCCTGCTGAAATGCG 3 00

QY 499 CAGCTTGGCGGAGTGTGGCAACCCAGAGTTTGGCCAAACCCAGAGTT 5 58
Db 301 CAGCTTGGCGGAGTGTGGCAACCCAGAGTTTGGCCAAACCCAGAGTT 3 60

QY	619	GTTTGGGAAATCCACCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGC	678	1699 CCTAACATCAAGGATCTGCCACTTGTGCTGACCCGCTGAAAGCAGCTGGC 1758	
Db	421	GTTTGGGAAATCCACCCGAGCAAAAACATCGATGAGATCGTTAAAAGCGCTGAAGGC	480	1501 CCTAACATCAAGGATCTGCCACTTGTGCTGACCCGCTGAAAGCAGCTGGC 1560	
QY	679	CAGACTACCCCATCTTGTGAAGGGAGTTGGCTGGGACGGGATCGTTAAAAGCGCTGAAGGC	738	1759 CCAGCCGGTTTGCTCTGCTGACTTCGCACTGGCAGTCGGCAGTCGGCAGTCGGCT 1818	
Db	481	CAGACTACCCATCTTGTGAAGGGAGTTGGCTGGGACGGGATCGTTAAAAGCGCTGAAGGC	540	1561 CCAGCCGGTTTGCTCTGCTGACTTCGCACTGGCAGTCGGCAGTCGGCAGTCGGCT 1620	
QY	739	GTTGCTTCACTGTAGCTGGCAATTAGAACAGAAGGATCTGTGAAGGTGAAGGC	798	1819 TTCCCGATGCAACACCAAGTCTTGTGCTGGCACGTCGGCTCATTCGACTGAAGGC	1878
Db	541	GTTGCTTCACTGTAGCTGGCAATTAGAACAGAAGGATCTGTGAAGGTGAAGGC	600	1621 TTCCCGATGCAACACCAAGTCTTGTGCTGGCACGTCGGCTCATTCGACTGAAGGC	1680
QY	799	GCTTTGGCATGGCTGGGATGAGCTGGCTGGGATGACCTCGGATATTGAA	858	1879 GCGGAGAGGGCGTGCACAAAGCTGACTCTGTGAGCTTTGTCCGTGGGAGCTGGG 1938	
Db	601	GCTTTGGCATGGCTGGGATGAGCTGGCTGGGATGACCTCGGATATTGAA	660	1681 GCGGAGAGGGCGTGCACAAAGCTGACTCTGTGAGCTTTGTCCGTGGGAGCTGGG 1740	
QY	859	GTGAGATCCTGGGATCACACTGGGAGGTTGACACCTTATGAACTGCTCA	918	1939 GCGAACCTACGATGTTGGGATGCGTTCTCTGTGAGATCCCTGGGAGCTGGCTGACAGG	1998
Db	661	GTGAGATCCTGGGATCACACTGGGAGGTTGACACCTTATGAACTGCTCA	720	1741 GCGAACCTACGATGTTGGGATGCGTTCTCTGTGAGATCCCTGGGAGCTGGCTGACAGG	1800
QY	919	CTGCAGGTGTCACCAAAGTGTGAAATTGGGATCCAGAA	978	1999 CTGGCGAGGGGATGCCGATGGCTGCTGCTGCTTCCGGCCAAACACCGTG	2058
Db	721	CTGCAGGTGTCACCAAAGTGTGAAATTGGGATCCAGAA	780	1801 CTGGCGAGGGGATGCCGATGGCTGCTTCCGGCCAAACACCGTG 1860	
QY	979	CTGGGTGATGCCATTGGGATGGAGTAAGTTCTGGCCTCCATTGGTACAGGGC	1038	1861 GGATACACCCGGTACCGAGACTCCGTCGACCGGCTTAACGACGTTCCAGCA	2118
Db	781	CTGGGTGATGCCATTGGGATGGAGTAAGTTCTGGCCTCCATTGGTACAGGGC	840	2119 GGATACACCCGGTACCGAGACTCCGTCGACCGGCTTAACGACGTTCCAGCA	2178
QY	1039	GCGGAAACCGGGGATCTTGGTGGATGAAAGGGCAACCACCGTCTCATCGAAATGAA	1098	1980 GGCGTGGACATCTTCCGGATCTTCGACCGGCTTAACGACGTTCCAGATGCGTCCAGCA	2238
Db	841	GCGGAAACCGGGGATCTTGGTGGATGAAAGGGCAACCACCGTCTCATCGAAATGAA	900	1981 ATCGAGCCGGTACCCGGGATGCCAACACCGGGTAGCCGGCTATGGCTTAACTCTGTT	1920
QY	1099	CAAGTATCCAGGTGAGCACCCGGGAAACCTGGGACCTGGTGAAG	1158	1982 GATCTCTCTGATCCAATGAAAAGCTCTACACCCGGGATTAACCTACCTACCTGGATTACTACCTAAAGATGGCAGAG	2040
Db	901	CAAGTATCCAGGTGAGCACCCGGGAAACCTGGGACTGGGACCTGGTGAAG	960	2041 GATCTCTCTGATCCAATGAAAAGCTCTACACCCGGGATTAACCTACCTGGATTACTACCTAAAGATGGCAGAG	2100
QY	1159	GCGCAGATGGCTGGCTGGTGGCAACCTGAAAGGAAATTGGGTCTGACCCAAGATAAG	1218	2239 GAGATGTCAAAGTCTGGGCTCACATCTTGGCCATTAAAGGATATGGCTGTCRGTCTGC 2298	
Db	961	GCGCAGATGGCTGGCTGGTGGCAACCTGAAAGGAAATTGGGTCTGACCCAAGATAAG	1020	2240 GATCTCTCTGATCCAATGAAAAGCTCTACACCCGGGATTAACCTGGATTACTACCTAAAGATGGCAGAG	2160
QY	1219	ATCAAGACCCACGGGAACTATCACCGGTGAGCGACTCGAGTGGCCATCACCCACGGC	1278	2241 GCGGACACCCACGGGAACTGCGGCTCCGGCAAGCTGGCTCAAGCT 2358	
Db	1021	ATCAAGACCCACGGGAACTATCACCGGTGAGCGACTCGAGTGGCCATCACCCACGGC	1080	2101 GAGATGTCAAAGTGGCTCACATCTGGCCATTAAAGGATATGGCTGAATTGCGTCAAGTCGTC 2220	
QY	1279	TTCGGCCAGATAACGGGAACTATCACCGGTGAGCGACTCGAGTGGCCATCACCCACGGC	1338	2359 CCAGCTGGGTAACCAAGCTGGTCAACCGGACTGGCTGCTGGCAGTCGGCTCAAGCT 2418	
Db	1081	TTCGGCCAGATAACGGGAACTATCACCGGTGAGCGACTCGAGTGGCCATCACCCACGGC	1140	2161 CCAGCTGGGTAACCAAGCTGGCTCACATCTGGCCATTAAAGGATATGGCTGAATTGCGTCAAGTCGTC 2478	
QY	1339	CTTGACGGCAGTCAGCTGGCTGGGAAATTCAACCGGAACTTGTGACTCCATGCTGGT	1398	2419 GGTGAGATGGCTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2280	
Db	1141	CTTGACGGCAGTCAGCTGGCTGGGAAATTCAACCGGAACTTGTGACTCCATGCTGGT	1200	2221 GTGCAACCCACGGGACTGGCTGTTGCTGCACTTCGGGCAACCTACTTTGCTGCAAGTCGTC 2280	
QY	1399	AAAATGACCTGGCTGGGAAATTCAACCGGAACTTGTGACTCCATGCTGGT	1458	2479 GGTGAGATGGCTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2538	
Db	1201	AAAATGACCTGGCTGGGAAATTCAACCGGAACTTGTGACTCCATGCTGGT	1260	2281 GTGCAAGATGGCTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2340	
QY	1459	GCTGAGGTTACCGGTGCTGGTGTGCAACCGAACATTGGTTCTTGTGCTGCTGCTGGT	1518	2539 CTGCTGCCATTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2598	
Db	1261	GCTGAGGTTACCGGTGCTGGTGTGCAACCGAACATTGGTTCTTGTGCTGCTGGT	1320	2341 CTGCTGCCATTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2400	
QY	1519	GAAGAGGACCTTCACTTCCAAAGGGATTATGCCGATCACCCGCACCTC	1578	2599 GCTGCTGCCATTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2658	
Db	1321	GAAGAGGACCTTCACTTCCAAAGGGATTATGCCGATCACCCGCACCTC	1380	2401 GCTGCTGCCATTGTTGCTGCACTTCGGGCAACCCGGGACTGGCTCAAGCT 2460	
QY	1579	CTTCAGGGTCCACCTGGCTGATGAGTGGGAGCGCATCTGGATTACTGGAGATGTC	1638	2659 TCTGGAACCCAGGGCAACCCGGTCTACCGGCCACGGCAACTGGCTCAAGCT 2718	
Db	1381	CTTCAGGGTCCACCTGGCTGATGAGTGGGAGCGCATCTGGATTACTGGAGATGTC	1440	2461 TCTGGAACCCAGGGCAACCCGGTCTACCGGCCACGGCAACTGGCTCAAGCT 2520	
QY	1639	ACCGTGAACAAAGCCTCATGGTGTGCTCAAGGATGTGCACTGGCTTATCGATAAGCTG	1698	2719 TCCAACCTGGCTGCAAGGGCACTGGGCTTGGGATCGTTCAAGCT 2778	
Db	1441	ACCGTGAACAAAGCCTCATGGTGTGCTCAAGGATGTGCACTGGCTTATCGATAAGCTG	1500	2521 TCCAACCTGGCTGCAAGGGCACTGGGCTTGGGATCGTTCAAGCT 2580	
QY	2779	GACAACACTCGGAGCCGTTAATGAGATGCTGGGACGCCAACCAAGGTCAACCA	2838	2779 GACAACACTCGGAGCCGTTAATGAGATGCTGGGACGCCAACCAAGGTCAACCA	

Qy	1108	CAGGTGAGCAACCGTGAACGGTGAACGAAAGTACCGAGGTGACCTGGTGAAGGGCAGATG	1167	2188 GTCCTGGAGACCAACCCGGTAGCCGAGGGCTATGGCTTATTCTGGTGTATCTCTCT 2247
Db	961	CAGGTGAGCAACCGTGAACGGTGAACGAAAGTACCGAGGTGACCTGGTGAAGGGCAGATG	1020	2041 GTCCTGGAGACCAACCCGGTAGCCGAGGGCTATGGCTTATTCTGGTGTATCTCTCT 2100
Qy	1168	CCCTTGCTGGTCAACCTGAGGAACTTGGGACTGGCTAACGAAAGATAAGATCAAAGACC	1227	2248 GATCCAATGAAAAGCTCACCCCTGGATTACTACCTAACCTGGAGGAGATCGTC 2307
Db	1021	CGCTTGGCTGCTGGTCAACCTGGGAACTTGGGCTAACGAAAGATAAGATCAAAGACC	1080	2101 GATCCAATGAAAAGCTCACCCCTGGATTACTACCTAACCTGGAGGAGATCGTC 2160
Qy	1228	CACGGTGCAGGCACTGGCACTGGCATCACCAAGGAAGATCCAAACAAACGGCTTCGGCCA	1287	2308 AAGTCTGGGCTCACATCTGGCCATTAAAGGATAAGGATTAAGGATGGCTGGTGGCG 2367
Db	1081	CACGGTGCAGGCACTGGCAATCACCAAGGAAGATCCAAACAAACGGCTTCGGCCA	1140	2161 AAGTCTGGGCTCACATCTGGCCATTAAAGGATGGCTGGTGGCG 2220
Qy	1288	GATAACGGAACTATCACCGGTACCGGTACAGGGTCAACAGGGGAGCTGGCTGACGGT	1347	2368 GTAACCAAGCTGGCAACCTGGCACTGGCAGTGCATCTGGTGAACACC 2427
Db	1141	GATAACGGAACTATCACCGGTACCGGTACAGGGGAGCTGGCTGACGGT	1200	2221 GTAACCAAGCTGGTACCCGACTGGCCAGTTGGCTAACCTGGTGAATCGTGCACACC 2280
Qy	1348	GCAGCTAGCTGGTGGAAATCACCGGACAACCTTGACTCCATGCTGGTAAATGACC	1407	2428 CACGACACTGGGCTGGCCAGCTGGCAACCCACTGTCTGGCACCCAGCTCCAGGCCATCCCTGTCG 2487
Db	1201	GCAGCTAGCTGGTGGAAATCACCGGACAACCTTGACTCCATGCTGGTAAATGACC	1260	2281 CACGACACTGGGCTGGCCAGTTGGCTAACCTGGTGAATCGTGCAGGAT 2340
Qy	1408	TGCGGTGTTCCGACTTTGAAACACTGGTGTGGCTCGTGGTGGTGGTGAAGTT	1467	2488 GCTGTTGACGGTGCCTGGCAGCTGGCAACCCACTGTCTGGCACCCAGCTCCAGGCCATCCCTGTCG 2547
Db	1261	TGCGGTGTTCCGACTTTGAAACACTGGTGTGGCTCGTGGTGAACGGGGTGGTGAAGTT	1320	2341 GCTGTTGACGGTGCCTGGCAGACCCGTGGTGGGATACGGTTTGGCTTCT 2400
Qy	1468	ACCGTGTCTGGTGTGTTGAAACCAACATTGGTTCTTGGTGGTGGTGGTGGAGGAC	1527	2548 ATTGTTGCTGCATTTCGGCAACCCGTGGTGGGATACGGTTTGGCTTCT 2607
Db	1321	ACCGTGTCTGGTGTGTTGAAACCAACATTGGTTCTTGGTGGTGGAGGAGGAC	1380	2401 ATTGTTGCTGCATTTCGGCAACCCGTGGTGGGATACGGTTTGGCTTCT 2460
Qy	1528	TTCACCTCCAAGGGCATCGGCCATTGGCGATCACCGGACCTCCCTCAGGCT	1587	2608 GACCTCGAGGCCGTACTGGGAGGCACTGGTGCCTGGGACTTGGCATTTGAGTCCTGGAACCC 2667
Db	1381	TTCACCTCCAAGGGCATCGGCCACCGGATTATCGGCCACGGGATCACCTCCCTCAGGCT	1440	2461 GACCTCGAGGCCGTACTGGGAGGCACTGGTGCCTGGGACTTGGCATTTGAGTCCTGGAACCC 2520
Qy	1588	CAACCTGGTGTGATGATGAGCAGGGGACCGCATCTGGGATTACCTGGCAGATGTCAACGTGAAC	1647	2668 CCAGGCCAACCCGGTGCCTGCTACCGGCCACGAATCCAGGGGACAGTGTGTCCTGGAACCTG 2727
Db	1441	CAACCTGGTGTGATGATGAGCAGGGGACCGCATCTGGGATTACCTGGCAGATGTCAACGTGAAC	1500	2521 CCAGGCCAACCCGGTGCCTGCTACCGGCCACGAATCCAGGGGACAGTGTGTCCTGGAACCTG 2580
Qy	1648	AAGCCTCATGGTGTGCTCCAAAGGGATGGTCCATGGCTTATGATAAGCTGCCAACATC	1707	2728 CGTGACAGGCCACCGGACTGGCCCTGGGATCTGGGACTCATGGAAAGACAATAC 2787
Db	1501	AAGCCTCATGGTGTGCTCCAAAGGGATGGTCCATGGCTTATGATAAGCTGCCAACATC	1560	2581 CGTGACAGGCCACCGGACTGGCCCTGGGATCTGGGACTCATGGAAAGACAATAC 2640
Qy	1708	AGGATCTGCCACTGCTGATCTCCGTGAGGAGCTGGCAGCAATCGTAACTGGGATCTGGCAGGAT	1767	2788 GCAGCCGTTAATGAGATGCTGGGACGCCAACCAAGGTCAACCCATCCTCCAGGTGTT 2847
Db	1561	AGGATCTGCCACTGCTGATCTCCGTGAGGAGCTGGCAGCAATCGTAACTGGGATCTGGCAGGAT	1620	2641 GCAGCCGTTAATGAGATGCTGGGACGCCAACCAAGGTCAACCCATCCTCCAGGTGTT 2700
Qy	1768	TTTGTCTGGTGAACGGCTTCCGGTGAACGGGACTGGCAGCACTGGCAGTACTGATAACCCTTCCGGAT	1827	2848 GGCACCTCGCACTCCACCTGGGACTTGGCTCATGGCTTCCGGGAGCTGGTGGTAAC 2907
Db	1621	TTTGTCTGGTGAACGGCTTCCGGTGAACGGGACTGGCAGCACTGGCAGTACTGATAACCCTTCCGGAT	1680	2701 GGCAACCTCGCACTCCACCTGGGACTTGGCTCATGGCTTCCGGGAGCTGGTGGTAAC 2760
Qy	1828	GCAACCCAGTCTGGCTCATTCGGCAGTCACTGGCAGGACTGGCAGCTGGCAGGAG	1887	2908 CCACAAAGTAGACATCCAGACTCTGGCTCATGGCTTCCGGGAGCTGGTGGTAAC 2967
Db	1681	GCAACCCAGTCTGGCTCATTCGGCAGGACTGGCAGCTGGCAGGAGCTGGCAGGAG	1740	2761 CCACAAAGTAGACATCCAGACTCTGGCTCATGGCTTCCGGGAGCTGGTGGTAAC 2820
Qy	1888	GCGTGCACAAAGCTGACTCTGGCTGGCTGGCGGGCACCTAC	1947	2968 CCTCAGGGCTGGCCAGGCACTGGCACCCGGGACTGGCACCCGGCTGGGAGCTGGCACCC 3027
Db	1741	GCGTGCACAAAGCTGACTCTGGCTGGCTGGCGGGCACCTAC	1800	2821 CCTCAGGGCTGGCCAGAACCCGGGACTGGCACCCGGCTGGGAGCTGGCACCC 2880
Qy	1948	GATGTGGGATGGCTTCTCTCTGGGATCCGGGACTGGGAGCTGGCAGGAG	2007	3028 AAGGCAACCTCTGGGACTCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3087
Db	1801	GATGTGGGATGGCTTCTCTGGGATCCGGGACTGGGAGCTGGCAGGAG	1860	2881 AAGGCAACCTCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 2940
Qy	2008	GCGATGCCAATGTAACATTGATGCTGCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 2067		3088 AAGGCAACCTCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3147
Db	1861	GCGATGCCAATGTAACATTGATGCTGCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 1920		2941 AAGGCAACCTCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3000
Qy	2068	CCGTACCCAGACTCCGTCTGGCCAAACACTCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 2127		3148 GAGGACCGTGCAGGGCCGAGACTTGGCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3207
Db	1921	CCGTACCCAGACTCCGTCTGGCCAAACACTCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 1980		3208 CTGGTGGAGCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3120
Qy	2128	ATCTTCCGCATCTTGCAGCGCTTAACGACCTCCAGATGGTCCAGCAATCGACGCA	2187	3061 CTGGTGGAGCTGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCCGGCTGGGAGCTGGCACCC 3327
Db	1981	ATCTTCCGCATCTTGCAGCGCTTAACGACCTCCAGATGGTCCAGCAATCGACGCA	2040	3268 CGCTCTGGATGGATCTGAGCCAGAGGATAAGGGTATGGGCAATGGCCAAACCGTC 3327

Db	3121	CGCTGGATGCGATCTGTAGCCAACTGGCTCGGTGAGTCACCGCAACC	3180	Db	361	CGCGAGTGCAGGGAAACGGCATTACTTTATGGCCAACCCAGAGGTCTTGATCTC	420
Qy	3328	AACGCCAGATCGCCCAATGGCTCGGTGAGTCACCGCAACC	3387	Qy	568	ACCGGTGATAAGTCTCGCGGGTAACGCCAGGCTGGCTGGCTGGCG	627
Db	3181	AACGCCAGATCGCCCAATGGCTCGGTGAGTCACCGCAACC	3240	Db	421	ACCGGTGATAAGTCTCGCGGGTAACGCCAGGCTGGCTGGCTGGCG	480
Qy	3388	GCAGAAAGGCCAGATCCTCAACCAAGGGCAGTGGCACCATTCGCTGGTGC	3447	Qy	628	GAATCCACCCGGAAACATCGATGAGATCGTTAACAGCGCTGAAGGCCAGACTTAC	687
Db	3241	GCAGAAAGGCCAGATCCTCAACCAAGGGCAGTGGCACCATTCGCTGGTGC	3300	Db	481	GAATCCACCCGGAAACATCGATGAGATCGTTAACAGCGCTGAAGGCCAGACTTAC	540
Qy	3448	ACCGTGACTGTGCTGAAGGTGAGTCAGGTCAAAGCTCATCGAG	3507	Qy	688	CCCATCTTGTGAAGGCCAGTCTCGTGAAGCTGAAGGGCTTCGGC	747
Db	3301	ACTGTGACTGTGCTGAAGGTGAGTCAGGTCAAAGCTCATCGAG	3360	Db	541	CCCATCTTGTAAAGGCCAGTCTCGTGAAGCTGAAGGGCTATCGGC	600
Qy	3508	GCTATGAAAGCAACATCACTGCTCTGTTGACGGTCAAGTCAGTCATCGAG	3567	Qy	748	CCTGATGAGCTTCGCAAAATTAGAACAGAAGGATCTCGTGAAGCTGAAGGGCTTCGGC	807
Db	3361	GCTATGAAAGCAACATCACTGCTCTGTTGACGGTCAAGGTGAGTCATCGAG	3420	Db	601	CCTGATGAGCTCCGCAAATTGGCAACAGAAGGATCTCGTGAAGCTGAAGGGCTATCGGC	660
Qy	3568	GTTCCTGCTGCAACGAAAGGTGGCAACTGATCGTCGTTCTCCTAA	3621	Qy	808	GATGGCGGGTATATGTCGAACTGCTGCTGATTAACCTCTAGGATATGAAAGTCAGATC	867
Db	3421	GTTCCTGCTGCAACGAAAGGTGGCAACTGATCGTCGTTCTCCTAA	3474	Db	661	GACGGTTGGATGCAACTGTCGTTGATTAACCCCAGACATGAAAGTCAGATC	720
Qy	868	CTTGGCGATCACACTGGAAAGTTGACACCTTATGAAACCTGACTGCTCACTGGAGCGT	927	Qy	868	CTTGGCGATCACACTGGAAAGTTGACACCTTATGAAACCTGACTGCTCACTGGAGCGT	927
Db	721	CTTGGCGATTCGCACTGGAAAGTTGACACCTTATGAAACCTGACTGCTCACTGGAGCGT	780	Db	721	CTTGGCGATTCGCACTGGAAAGTTGACACCTTATGAAACCTGACTGCTCACTGGAGCGT	780
Qy	928	CGTCACCAAAAGTGTGCAAATTGGCGCAGCACGATTGGATCCGAAACTGCGTGTGAT	987	Qy	928	CGTCACCAAAAGTGTGCAAATTGGCGCAGCACGATTGGATCCGAAACTGCGTGTGAT	987
Db	781	CGTCACCAAAAGTGTGCAAATTGGCGCAGCACGATTGGATCCGAAACTGCGTGTGAT	840	Db	781	CGTCACCAAAAGTGTGCAAATTGGCGCAGCACGATTGGATCCGAAACTGCGTGTGAT	840
Qy	988	CGCATTGTCGGATGGCATAAGTCTGCCGCTCCATTGGTTACCGGGGGGGAAACC	1047	Qy	988	CGCATTGTCGGATGGCATAAGTCTGCCGCTCCATTGGTTACCGGGGGGGAAACC	1047
Db	841	CGCATTGTCGGATGGCATAAGTCTGCCGCTCCATTGGTTACCGGGGGGGAAACC	900	Db	841	CGCATTGTCGGATGGCATAAGTCTGCCGCTCCATTGGTTACCGGGGGGGAAACC	900
Qy	1048	GTGGAATTCTGGTGTGATGAAAGGCAACCACGTCTCATCGAAATGAAACCACGTATC	1107	Qy	1048	GTGGAATTCTGGTGTGATGAAAGGCAACCACGTCTCATCGAAATGAAACCACGTATC	1107
Db	901	GTGGAATTCTGGTGTGATGAAAGGCAACCACGTCTCATCGAAATGAAACCACGTATC	960	Db	901	GTGGAATTCTGGTGTGATGAAAGGCAACCACGTCTCATCGAAATGAAACCACGTATC	960
Qy	1108	CAGGTGAGCACACCGTGTACTGAAAGAAGTCAAGGAGGTGGCACTTGGTAAGGGCGAGATG	1167	Qy	1108	CAGGTGAGCACACCGTGTACTGAAAGAAGTCAAGGAGGTGGCACTTGGTAAGGGCGAGATG	1167
Db	961	CAGGTGAGCACACCGTGTACTGAAAGAAGTCAAGGAGGTGGCACTTGGTAAGGGCGAGATG	1020	Db	961	CAGGTGAGCACACCGTGTACTGAAAGAAGTCAAGGAGGTGGCACTTGGTAAGGGCGAGATG	1020
Qy	1168	CGCTTGGCTGCTGCACCTTGAAACCTTGAAAGGAAATTGGGTCTGACCCAAAGATCAAGACC	1227	Qy	1168	CGCTTGGCTGCTGCACCTTGAAACCTTGAAAGGAAATTGGGTCTGACCCAAAGATCAAGACC	1227
Db	1021	CGCTTGGCTGCTGCACCTTGAAACCTTGAAAGGAAATTGGGTCTGACCCAAAGATCAAGACC	1080	Db	1021	CGCTTGGCTGCTGCACCTTGAAACCTTGAAAGGAAATTGGGTCTGACCCAAAGATCAAGACC	1080
Qy	1428	GTGACTGCTATCACCTTGGGTCCTTGTGAAAGGAATAATTACTCTAGTGTGCACT	207	Qy	1228	CACGGTGCAGGACTGCACTGGCTACCCAGGAAGATCCAAACAAAGGCTTCGGCCCA	1287
Db	1	GTGACTGCTATCACCTTGGGTCCTTGTGAAAGGAATAATTACTCTAGTGTGCACT	60	Db	1081	CACGGTGCAGGACTGCACTGGCTACCCAGGAAGATCCAAACAAAGGCTTCGGCCCA	1140
Qy	208	CACACATCTCAACGCTTCAGGTCAGGCACTCGTCAACGGTAAACCGGGGAATTC	267	Qy	1288	GATACCGGAAACTATCACCGCGTACCCGGCTCACCGGTACCGCTCACCGGGAGCTGGGT	1347
Db	61	CACACATCTCAACGCTTCAGGTCAGGCACTCGTCAACGGTAAACCGGGGAATTC	120	Db	1141	GATACCGGAAACTATCACCGCGTACCCGGCTCACCGGGAGCTGGGT	1200
Qy	268	GCGGTCCGTCGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC	327	Qy	1348	GCAGCTCAGCTGGTGGGAAATCACGGCACACTTGTGAAACATGCTGGTAAATGACC	1407
Db	121	GCGGTCCGTCGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC	180	Db	1201	GCAGCTCAGCTGGTGGGAAATCACGGCACACTTGTGAAACATGCTGGTAAATGACC	1260
Qy	328	CCTGAAAGATCGGGGATCACTCCACCGGTCCTTGTGAAAGCTGTGGTACC	387	Qy	1408	TGCCGTGGTTGCACCTTGAAACTTGCTGGCTGCTGCGCAAGGGAAAGAGGAC	1467
Db	181	CCTGAAAGATCGGGGATCACTCCACCGGTCCTTGTGAAAGCTGTGGTACC	240	Db	1261	TGCCGTGGTTGCACCTTGCTGGCTGCTGCGCAAGGGAAAGAGGAC	1320
Qy	388	GAAGGCTACCAAGTCAGGTCAGGTAACCTGGACATCGTGAAGAATTACGGTCAAGCTAAAAA	447	Qy	1468	ACCGTGTCTGGTCAACCAACATGGCTGGCTGCTGCGCACTCCCTTAGGCT	1587
Db	241	GAAGGCTACCAAGTCAGGTCAGGTAACCTGGACATCGTGAAGAATTACGGTCAAGCTAAAAA	300	Db	1321	ACCGTGTCTGGTCAACCAACATGGCTGGCTGCTGCGCACTCCCTTAGGCT	1380
Qy	448	GTTAAAGGCAATGATGAGTCATCTGGGAGATCGCTGGCTGAAATGCCCAAGCTTGC	507	Qy	1528	TTCACCTCCAGGGATTCATGGCTGGCTGCTGCGCACTCCCTTAGGCT	1440
Db	301	GTTAAAGGCAATGATGAGTCATCTGGGAGATCGCTGGCTGAAATGCCCAAGCTTGC	360	Db	1381	TTCACCTCCAGGGATTCATGGCTGGCTGCTGCGCACTCCCTTAGGCT	1647
Qy	508	CGCGAGTGTGGAAAACGGCATTACTTTATTGGCCAACCCAGAGGTTCTGATCTC	567	Qy	1588	CCACCTGCTGATGAGTCATCTGGGAGATCGCTGGCTGAAATGCCCAAGCTTGC	567

RESULT 5

US-09-974-973-3

; Sequence 3, Application US/09974973

; Patent No. US2002017202A1

; GENERAL INFORMATION:

; APPLICANT: Hanke, Paul D.

; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacterium

; FILE REFERENCE: 1533.123001/MAC/RGM

; CURRENT APPLICATION NUMBER: US/09/974,973

; CURRENT FILING DATE: 2001-10-21

; PRIOR APPLICATION NUMBER: US 60/239,913

; PRIOR FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 3

; LENGTH: 3474

; TYPE: DNA

; ORGANISM: Corynebacterium glutamicum

; US-09-974-973-3

Query Match 93.9%; Score 3398.8; DB 9; Length 3474;

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 47; Indels 0; Gaps 0;

Matches 3427; Conservative 0; Gaps 0;

Qy 148 GTGACTGCTATCACCTTGGGTCCTTGTGAAAGGAATAATTACTCTAGTGTGCACT

Db 1 GTGACTGCTATCACCTTGGGTCCTTGTGAAAGGAATAATTACTCTAGTGTGCACT

Qy 208 CACACATCTCAACGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC

Db 61 CACACATCTCAACGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC

Qy 268 GCGGTCCGTCGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC

Db 121 GCGGTCCGTCGCTTCAGGTCAGGCACTCGTCAACGGTCACTTGTGAAAGCTGTGGTACC

Qy 328 CGTGAAGATCGGGGATCACTCCACCGGTCCTTGTGAAAGCTGTGGTACC

Db 181 CGTGAAGATCGGGGATCACTCCACCGGTCCTTGTGAAAGCTGTGGTACC

Qy 388 GAAGGCTACCAAGTCAGGTCAGGTAACCTGGACATCGTGAAGAATTACGGTCAAGCTAAAAA

Db 241 GAAGGCTACCAAGTCAGGTCAGGTAACCTGGACATCGTGAAGAATTACGGTCAAGCTAAAAA

Qy 448 GTTAAAGGCAATGATGAGTCATCTGGGAGATCGCTGGCTGAAATGCCCAAGCTTGC

Db 301 GTTAAAGGCAATGATGAGTCATCTGGGAGATCGCTGGCTGAAATGCCCAAGCTTGC

Qy 508 CGCGAGTGTGGAAAACGGCATTACTTTATTGGCCAACCCAGAGGTTCTGATCTC

Db	1441	CACCTGGGATCATGAGGGAGCATCCGGATTACTTGGAGATGTCAACCGTGAAC	1500	Qy	2728	CGTGCCACAGGCCACCGCAGCTGGGCATCGGCTTGAAACTCATGAGACAAC	2787
Oy	1648	AAGCCTCATGGTGGCTCAAAGGATGGCTGAGCTTATCGATAAGTCACATC	1707	Db	2581	CGTGCACAGGCCACCGCAGCTGGCTTGAGCTCATGAGACAAC	2640
Db	1501	AAGCCTCATGGTGGCTCAAAGGATGGCTGAGCCATCGATAAGTCACATC	1560	Qy	2788	GCAGGGCGTTAATGAGATGGTGGGACGCCAACCAAGGTCACTCCAAAGGTTGTT	2847
Oy	1708	AGGATCTGCCACTGCCACGGGTTCCCGTGACCGCCTGAAGGAGCTGGCCAGC	1767	Db	2641	GCAGGGCGTTAATGAGATGGTGGGACGCCAACCAAGGTCACTCCAAAGGTTGTT	2700
Db	1561	AGGATCTGCCACTGCCACGGGTTCCCGTGACCGCCTGAAGGAGCTGGCCAGC	1620	Qy	2848	GGCACCTCGCACTCCACCTCGTTGGGATCCAGGAGACTTGTGCCGGAT	2907
Oy	1768	TTTGCTCTGATCTCCGTGAGCCACTGGCAGCTGGCAGTTACTGATACACCTCCCGCAT	1827	Db	2701	GGCACCTCGCACTCCACCTGGCTCTGAGCTTCAGACCTTGTGZAGAC	2760
Db	1621	TTTGCTCTGATCTCCGTGAGCCACTGGCAGTTACTGATACACCTCCGGCAT	1680	Qy	2908	CCACAAAAGTAGACATCCAGACATCCAGACCTCCAGACTCTGTCA	2967
Oy	1828	GCACACAGCTGGCTGAGCCGAGTCCACTGAAGCTGGCAGAG	1887	Db	2761	CCACAAAAGTAGACATCCAGACATCCAGACCTCCAGACTCTGTCA	2820
Db	1681	GCACACAGCTGGCTGAGCCGAGTCCACTGAAGCTGGCAGAG	1740	Qy	2968	CCTCAGGTGGCTGGCCACTGGGCCACTGGCAAGGCCCTCCGAAGGGC	3027
Oy	1888	GCGCTGGCAAGGTCAGCTCTGAGCTGGCAGGCGGCCACCTAC	1947	Db	2821	CCTCAGGTGGCTGGCCAGGCGCACTGGCACCCGGCACTGGAAAGGGCG	2880
Db	1741	GCGCTGGCAAGGTCAGCTCTGAGCTGGCAGGCGGCCACCTAC	1800	Qy	3028	AAGGACACCTCTGACGAAAGTTCCTGAGGAAGGAGGGCACTCGGCAC	3087
Oy	1948	GATGTTGGCAAGGTCAGCTCTGAGCTGGCAGGCTGCGGAG	2007	Db	2881	AAGGACACCTCTGACGAAAGTTCCTGAGGAAGGAGGGCACTCGGCAC	2940
Db	1801	GATGTTGGCAAGGTCAGCTCTGAGCTGGCAGGCTGCGGAG	1860	Qy	3088	AAGGAAACGTGCAATAGCCTCAACCGCTGCTGTTCCGAAGCCAAC	3147
Oy	2008	GGGATGCCGAATGTAACATTCAAGATGGCTGCTTCGGCCGGCAACACC	2067	Db	2941	AAGGAAACGTGCAACAGGCTCAACCGCTGCTGTTCCGAAGGAAAGT	3000
Db	1861	GGGATGCCGAATGTAACATTCAAGATGGCTGCTTCGGCCGGCAACACC	1920	Qy	3148	GAGCACCGTGCCTGGCAACACCTCTGCGCTGGATGATCGTGAATCTTACGGC	3207
Oy	2068	CGGTACCCAGAACTCCGTCGCGCCGCTCCGGCTGGAC	2127	Db	3001	GAGCACCGTGCCTGGCAACACCTCTGCGCTGGATGATCGTGAATCTTACGGA	3060
Db	1921	CGTACCCAGAACTCCGTCGCGCCGGCTGGAC	1980	Qy	3208	CTGGTGAAGGCCGCTCGCAGATGTCGCCACCTCGCTGTTGTT	3267
Oy	2128	ATCTTCCGATCTTCGACGGCTTAACGACGCTCTCCAAATCGACGCA	2187	Db	3061	CTGGTGAAGGCCGCTCGCAGATGTCGCCACCTCGCTGTT	3120
Db	1981	ATCTTCCGATCTTCGACGGCTTAACGACGCTCTCCAAATCGACGCA	2040	Qy	3268	CGCCCTGGATGGCAATCTGAGGCCAGACATAAGGTAATGGCAATGTTGGCCAAACGTC	3327
Oy	2188	GTCCTGGAGACCAACCCGGTACCCGAGGTGGCTATGGCTTATTCTGGTATCTCT	2247	Db	3121	CGCCCTGGATGGCAATCTGAGGCCAGACATAAGGTAATGGTATGGCAATGTC	3180
Db	2041	GTCCTGGAGACCAACCCGGTACCCGAGGTGGCTATGGCTTATTCTGGTATCTCT	2100	Qy	3328	AACGCCAGATCGCCCAATGCGCTCGGCTGACCGCTCGTTGAGTCACCGCAACC	3387
Oy	2248	GATCCAAATGAAAAGCTCTACCCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC	2307	Db	3181	AACGCCAGATCGCCCAATGCGCTGGGTGACCGCTCCGGTTGAGTC	3240
Db	2101	GATCCAAATGAAAAGCTCTACCCCTGGATTACTACCTAAAGATGGCAGAGGAGATCGTC	2160	Qy	3388	GCAGAAAAGGCCGATTCTCCAACAAAGGCCCATGTTGCTGCACCCATTGCTGGTGTGTC	3447
Oy	2308	AAGTCTGGGCTCACATCTGGCCATTAAAGGATATGGCTGGCTGGCTGG	2367	Db	3241	GCAGAAAAGGCCGATTCTCCAACAAAGGCCCATGTTGCTGGTGTGTC	3300
Db	2161	AAGTCTGGGCTCACATTCTGGCCATTAAAGGATATGGCTGGCTGG	2220	Qy	3448	ACCGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGATGCAATCATCGAG	3507
Oy	2368	GTAACCAAGGCTGGCTCACGGCACTGGCCATTGGCTGGCTGGCACACC	2427	Db	3301	ACGTGACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGATGCAATCATCGAG	3360
Db	2221	GTAACCAAGGCTGGCTCACGGCACTGGCCATTGGCTGGCACACC	2280	Qy	3508	GCTATGAAAGATGGCAAGCAACAAATCACTGCTTGTGAGTCATCGCTGGTGTG	3567
Oy	2428	CACGACACTGGGGTGGCTGGCAACCTACTTCCCTGGCTAACGCTGGCAGAT	2487	Db	3361	GCTATGAAAGATGGCAAGCAACAAATCACTGCTTGTGAGTCATCGCTGGTGTG	3420
Db	2281	CACGACACTGGGGTGGCTGGCAACCTACTTCCCTGGCTAACGCTGGCAGAT	2340	Qy	3568	GTTCTGCTGCAACGAAGGTGGAAAGGTCGGGACTTGTGATCGTC	3621
Oy	2488	GCTGTTGACGGCTGGCTGGCAACCTACTTCCCTGGCTAACGCTGGCAGAT	2547	Db	3421	GTTCTGCTGCAACGAAGGTGGAAAGGTCGGACTTGTGATCGTC	3474
Db	2341	GCTGTTGACGGCTGGCTGGCAACCTACTTCCCTGGCTAACGCTGGCAGAT	2400	Qy	2548	ATTGTTGCTGCAATTGGCAGACCCGGTGGCAATCCGGTGGCTGAGCTGTTCT	2607
Oy	2401	ATTGTTGCTGCAATTGGCAGACCCGGTGGCTGAGCTGTTCT	2460	Db	2608	GACCTCGAGGCCGTACTGGGAAGGAGCTGCGCCATTTGAGTCAGTGTGAAACC	2667
Db	2461	GACCTCGAGGCCGTACTGGGAAGGAGCTGCGCCATTTGAGTCAGTGTGAAACC	2520	Qy	2668	CGAGGCCAACGGGTGGCTAACGCCAACAAATCCAGGGGACAGTTGTCCAACCTG	2727
Oy	2521	CGAGGCCAACGGGTGGCTAACGCCAACAAATCCAGGGGACAGTTGTCCAACCTG	2580	Db	2521		

RESULT 6
US-10-282-122A-17701
; Sequence 17701, Application US/10282122A
; General Information:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282, 122A
; CURRENT FILING DATE: 2003-02-20
; PRIORITY FILING DATE: 2000-09-09
; PRIORITY FILING DATE: 2000-03-21
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY FILING DATE: 2000-05-26
; PRIORITY FILING DATE: 2000-03-23
; PRIORITY FILING DATE: 2000-09-06
; PRIORITY FILING DATE: 2000-05-23
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY FILING DATE: 2001-02-09
; PRIORITY FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 17701
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Corynebacterium diphtheriae
; US-10-282-122A-17701

Query Match 53.2%; Score 1927.4; DB 12; Length 3423;
Best Local Similarity 73.4%; Pred. No. 0; Indels 9; Gaps 2;
Matches 2494; Conservative 0; Mismatches 896;

Qy 213 ATCTTCAACGCTTCAGCATTCAGAAACGGATCTGGTAGCAAACCGGGGAATA CGGGT 272
Db 27 AACCTCTACGTTAACATCCATTGTCAAAGATCCTCGTTGTAACC GTGGAGATCGCCGT 86
Qy 273 CCGTGCTTCCGTCAGCACTTCACCGCTCTGGTAGCTTACCCCGGTGA 332
Db 87 GCGAGCTTTCTGTGAGCCTTGAACCGGTGCTACCGGTAGCTACCCGAACGA 146
Qy 333 AGATCGGGATCATTCACCGCTCTGGTAGCTTACCCCGGTGAAGG 392
Db 147 AGACCGTAATTCACTCCACGATCGTTGCTCTGATAATCGAGGAATCAACAAACGGG 206
Qy 393 CTACCAAGTCAGGGATACGGCTTCCTGTCTGAAATTATGGTAGCTAAAGTTAA 452
Db 207 ATCTGCGGTCAAAGGTACCTGATAATCGAGGAATCTCGTGTGCTAAACCAACGGG 266
Qy 453 AGCAGATGCCATTACCCGGATACGGCTTCCTGTCTGAAATTATGGTAGCTAAAGGG 512
Db 267 TGCCGACGCAATTACCCAGGTACGGCTACGGCTTCCTGTCTGAAACGGG 326
Qy 513 GTGTGCGGGAAAAGGCATTACTTTATTGGCCAAACCCAGGGTCTTGTGATCTCACCGG 572
Db 327 TGCGGTGAAACGGCATAAACCTTATCGGTCCACCTCCATCAGTGTGGAGCTTACCGG 386
Qy 573 TGATAAGTCTCGCGGGTAACCCGGGAAGGAAGGCTGGTGTGCCAGTTACCGG 632
Db 387 TGATAAAGCAGGTGCTGTTACCGGAGGGTGGCTGAGCTGAGAC 446
Qy 633 CACCCGAGCaaaaACATCGATGAGATCGTTAAAGGGCTGAAGGCCAGACTAACCCCAT 692
Db 1524 AGGTGAGCTACCGTCAACGTGGTCCCGTGAATCGCCTGCTGGGATTTGC 1583

Db 447 AGAGCCAAACGACGGATCCAAAGGAGGCTCGGAGAGCTGACCAAGGGGAGACCTTACCCGCT 506
Qy 693 CTTTGTGAAGGCCAGTGGCTGGGGACGGGTATGCTTGTGCTTACCTGA 752
Db 507 ATTCTCTAAAGCGTTGCCGGATGCTGGCTGGCGATGCCAGCGCCCGA 566
Qy 753 TGAGCTTGCCTAAATTAGCAACAGAACATCTCGTGAAGCTGAGCTGGATGG 812
Db 567 AAACCTAGAAAAGCTAGGAGCTGGCTCCCGTGAAGGGGGATGGATGG 626
Qy 813 CGGGTATATGTCGAACGTTGCTGTTAACCCTCAGGATATTGAAGTGGAGATCCCTGG 872
Db 627 CCGAGTCTACGCCAGGTGCTGAGCTTGAAGCTTGAATCCTCGAGATCCAGATCTGG 686
Qy 873 CGATCACACTGAGAAGTTGACACCTTATGAACTGACTGCTCACTGGCTGCTCA 932
Db 687 TGAATCCGGCTGCCAACATCATCCACCTGTACGGAGCTGTTGCTGGCCA 746
Qy 933 CCAAAAAGTTGTCGAATTGGCCAGCACGCAAGCAGGATTGGATCAGAAACTGCTGATGCGAT 992
Db 747 CCAAAGGTTGATGCGACTGCCCCAGCACAGCAAGCAGGATTGGATCAGGAAAGAT 806
Qy 993 TTGTCGGATGCGACTAAAGTTGTCGCTCCATTGGTTACCAAGGGGGAAACCGTGGAA 1052
Db 807 TTGTCGAGACGCGACTGCGGTTGACGGCACATCGTTACCAAGGTTGAGGCAAGGGTGCAGA 866
Qy 1053 ATTCTTGGTGTGATGAAAGGGCAACCCAGTCTGGTATCCAGGT 1112
Db 867 GTTCCTAGTGTGATGAGGAAGGGCAACACGTTCTCATCGAGATGAAACCTCTGTATCCAGGT 926
Qy 1113 TGAGCACACCGTGAAGTCAACGAGTCAACGGTTGACCTGGAAAGGGGAGATGGCGCTT 1172
Db 927 CGAACACACCGTGACCTGGTACCCAAAGTGGTACCCAGATCGTGAAGTCCAGATCATGAT 986
Qy 1173 GGCTGCTGGTGAACCTGCAACCCAGTCTGGTACCCAGTAAAGATCAAGACCCACGG 1232
Db 987 CGCTTCGGTGTGACACTCGAAAGGAGTCTCGAAAGAACATCCACACCGAAGG 1046
Qy 1233 TCGAGGCACTGCAACTGGCATCACCAGGAAGATCCAACAGGCTTCGGCCAGATAAC 1292
Db 1047 CGCTGCCCTGCACTGCGTATTACTACTGAAGACCCCACAAACGGTTTCGTCCTGACAC 1106
Qy 1293 CGGAACATCACCGGTACCGGTCAACAGGGGAGCTGGCTCGTCTGTGACGGTGCAGC 1352
Db 1107 CGAACGATTACCGCTTATCGTTCCCAAGGTGGCAGGTGTTGCTCGACGGTGTGTC 1166
Qy 1353 TCAGGCTCGGTGGCAGAAATACCGCAACACTTGTGACTCCATGGTGGAGCTGGCG 1412
Db 1167 CATGCTCGGTGAGATCACCCGAATTTCGACTCCATGCTGGTCAAGATGACCTGCCG 1226
Qy 1413 TGGTTCGGACTTGAACACTGGTGTGCTCGTGCAGGTCAACCGT 1472
Db 1227 TGGTGCCTGGTGTGCTGGCCACCGCACTGGCTCGGCTGAGTAACTCGTGTGT 1286
Qy 1473 GTCTGGTGTGTTGCAACCAACATGGTTCTTGCTGGTGTGGCTGGGGAAAGGGACTTCAC 1532
Db 1287 CTAGGGTGTGCTACCAAATCGGATTCCTGGATTCCTGGCTGCTGGCTGAGACTTCCA 1346
Qy 1533 TTCCAAAGGCATCGGCCACGGATTCACTGGCTCCTTCAGGGTCCACC 1592
Db 1297 GCACAAAGGCATCGGCCACGGATTCACTGGCTCCTTCAGGGTCCACC 1406
Qy 1593 TGGTGTGATGAGGCAAGGCTGGATTACTGGCTGGCTCCTTCAGGGTCCACC 1652
Db 1407 TGCCGACGATGAGCTGGCCGATTTGAACTCTAGCTGACTGTGACTGTGACT 1466
Qy 1653 TCACTGGTGTGGTCCAAAGGATGTTGCAAGCTCTTATCGATAAGCTGCCAACTCAAGGA 1712
Db 1467 TCACTGGTGTACGCCA--GCCGTGATCAACCCGGTAGAAAGCTCCAGGAGATCAA 1523
Qy 1713 TCTGCCACTGCGCACGCCGTTCCGTTGACGCCAGGGCTGGCTGGTTGC 1772
Db 1524 AGGTGAGCTACCGTCAACGTGGTCCCGTGAATCGCCTGCTGGGATTTGC 1583

Qy	1773	TCTGTATCTCGTGAAGGACGGCACTGGCAGTTACTGATAACCACCTTCGGCATGCCACA	1832	Qy	2853	CCTCCGCACTCCACCTCGTTGCGGGTGTGGATCCAGGAGACTTGTGCCATCCACA	2912
Db	1584	GCGCGCACTGGTAACACGGATGGCTCGGGTACGGATACCCCTCGGTGATGCCACA	1643	Db	2664	TCTTGCACTCTACCTAGTGGCAGGAGTTAACCCAGGGATCTTGAGCATCCCCA	2723
Qy	1833	CCAGCTTTGCTTGGCACCCGAGTCCGCTCATTCGCACTGAAGCTTGCGGAGGGCCGT	1892	Qy	2913	AAAGTAGCACATCCAGACTCTGTCACTGGTTCTGGAGCTGGTAACCCCTCC	2972
Db	1644	TCTAGTCGCTCTCGCAACCCGCTGGTCAACACGCTGATCGACGGACGGCACGT	1703	Db	2724	AAAGTAGATATTCTGACTCCGTCATGCCTTCCTCGTGGAGCTGGCACCCCTCC	2783
Qy	1893	CGCAAAGCTGACTCTTGTGAGCTTTGTCGGCTGGGGCGGCTACAGTGT	1952	Qy	2973	AGGTGGCTGGCCAGAGGCCACTGGCACCCGGGACTCTGGAAAGGGCAAGGGC	3032
Db	1704	CGCAAAGCTCACCCAGAGCTGCTCTGTAGAACATGGGGTGTGCTACATGACGT	1763	Db	2784	AGGGGGTGGCCAGAAAGAACCTGGTGTGCTGAGCTGATGATTCCAAAGGA	2843
Qy	1953	GGCGATGCGTTTCCTCTTGTAGGATTCGGTGGGATAACACCCCGTA	2012	Qy	3033	ACCTCTGACGGAAAGTTCCCTGGAGAAAGAGCAGGGCCACCTCGAACAGGA	3092
Db	1764	TGCTATGCGTTCCATGAGGACCCCTGGAGCGTCTGACCGACTCTGGGCCAT	1823	Db	2844	CACATTGGCCCCGCTGCCAGAGAAGATGAAGCTGAAAGCTGCAAGGACCC	2898
Qy	2013	GCGGAATGTAACACATTAGATGCTGCTTTCGCGGCAACACCCGGTA	2072	Qy	3093	ACGTRGCAATAGCCTAACCCGCTGCTGCTGGATGATCGTGAATTCTCTACGGCCTGGT	3152
Db	1824	GCCCCAACGTCAACATTAGTCAGTGGCTACACACCGTA	1883	Db	2899	-GTTGCCCCAACGGCTGCTTCCCAGAACGGTGTGGCAATTGGCTGAGAGCA	2957
Qy	2073	CCCGACTCGCTCGCGCTTACGGCTGGGACATCTT	2132	Qy	3153	CCGTRGCCGCTTGGCCAAACACCTCTGCTGGCAACTGGCAACGGCTGGCCT	3212
Db	1884	CCCAGATTCTGTATGCAAGGTTTGTGACAGTGTGCTGGTGTGATCTT	1943	Db	2958	CCGCCGTCAAGTTGGGATAACCCAAACTCGGTGCTGGCAATTGGCTTCAA	3017
Qy	2133	CCGCATCTTCGACGGCTTAACGAAGCTGGCCAGCTGGTGTGATCTT	2192	Qy	3213	CGAAGGGCCGGAGACTTTGATCGCCTGGCAGACTGGCACCCACTGCTGGCCT	3272
Db	1944	CCGCATCTTCGACGGCTTAACGAAGCTGGTGTGATCTGACGGAGTGCT	2003	Db	3018	AGAAGGCAAAGAACGGTCAATTGTACGGCAGACAGTAGCTGGTCCC	3077
Qy	2193	GGAGACCAACCCGGTAGCCACCCGATTACTACCTAACAGATGGCAGAGGAGATCGTC	2252	Qy	3273	GGATGGGATCTCTGAGCCAGGATAAGGGTATGGCAATGTGTGGCAATGTC	3332
Db	2004	CGAAACCAACACCAGATTGCCGAACTCCGGTACTCGGTGATCTGACCAACCC	2063	Db	3078	CGATGCCGTGGGAGCCGAGGAAAGGGCATGGCAACGGAAACGGTGTGCAACGG	3137
Qy	2253	AAATGAAAAGCTCACACCCGATTACTACCTAACAGATGGCTATGGTTAAGTC	2312	Qy	3333	CCAGATGCCCAATGCGTGTGGTGAACCGGCTCCGTGACCGAGA	3392
Db	2064	AAGTGGAGAACGCTCACACACTGGATTACTACCTAACAGCTGGGAAATCGTTAAGTC	2123	Db	3138	CCGAGATTGCCCATCTCGTGTGATGGCTAGAGTCAGTGGCACCATTGCTGGT	3197
Qy	2313	TGGGGCTCACATCTGGCCATTAGGATACTGGCTGGTGTGATCTGTAAC	2372	Qy	3393	AAAGGCAGATTCTCCAAACAGGGCCATTGCTGGTGTGACCGT	3452
Db	2124	CGGTGCACTGTTCTAGCCATTAAAGACATGGCTGGACTGTGATGAAAGGAAATCGTTAAGTC	2183	Db	3198	AAAGGCTGATCCCTCAACGGGACACGTAGCCGACATTGCTGTCAGCT	3257
Qy	2373	CAAGCTGGTCAACCGCACTGGCCAGCTGGCACACCCACGA	2432	Qy	3453	GACTGTTGCTGAAGGTGATGAGGTCAAGGCTGGAGATGCCATTGCAAT	3512
Db	2184	CAAGCTGGTCAACCGAACTACGACGGCAACTTGACCTGGCTACACCCACGA	2243	Db	3258	GACAATGAGGAAGGGCTAACGGTCAAAGCCGGCATCCAGGCTGTCAGT	3317
Qy	2433	CACTGCGGGTGGCCACCTACTTGTGGCAAGCTGGCAGATEGTGT	2492	Qy	3513	GAAGATGGAAAGCAAAATCACTGCTCTGTTGACGGCAAATGCTGGT	3572
Db	2244	CACTGCTGGTGGCCAGCTGGCTACGTATTGGCTGGGCAAGGCTGAGTCGGT	2303	Db	3318	GAAGATGGAGGAAAGGATCTGCCACCCAGGAAACGGTGTGACGAT	3377
Qy	2493	TGACGGTGGTCCGCCACCAACTGTGTGGCACCACTCCAGCCATCCCTGTCTGCCATTGT	2552	Qy	3573	TGCTGCAACGAGGTTGGCAACTTGATCTGCTGT	3611
Db	2304	CGATGGGCTCCGGCCACCTGGGACAACGTCGIAAGCCATCGTGTGTCAGGCAATTGT	2363	Db	3378	GCAGGCCACCAAGGTCGAAGGGAGCTGCTCTCGT	3416
Qy	2553	TGCTGCATTGGCAACCCGTGGGATACGGTTGAGGCTCTGGTGTGACCT	2612	RESULT 7			
Db	2364	GGCAGCATTGCTAACACCTACGGGATACGGCTCTCTGGACGTCGGATCGAT	2423	US-10-282-122A-25766			
Qy	2613	CGAGCGTACTGGGAAGGCAACTGGGGACTGTACCTGGCATTGGAGCTGGCTGC	2672	Sequence 25766, Application US/10282122A			
Db	2424	GAACACTGGCAACTGGGAACTCTACGGCAACCTACGGCCAGCTGTCGCGC	2483	GENERAL INFORMATION:			
Qy	2673	CCCAACGGTCTGGCTCATCCAGGAATCCGCACTGGGACTGTACCTGGCTGC	2732	APPLICANT: Wang, Liangbu			
Db	2484	ACCAACTGGCCGCTACGGCAACCTACGGCCAGCTGTCGCGC	2543	APPLICANT: Zudio, Carlos			
Qy	2733	ACAGGCCACGGCACTGGGACTGTGGGATCTGAAACTCATCGAAGGACAACTACGGCAGC	2792	APPLICANT: Malone, Cheryl			
Db	2544	ACAGGCAACTGCACTGGCTGGGAGCTACGGACTACTACGGCAGC	2603	APPLICANT: Haselbeck, Robert			
Qy	2793	C GTTAATGAGATGCTGGGGACGCCAACAAAGGTCAACCCCATCCTCCAGGTGTTGGCA	2852	APPLICANT: Ohlsen, Kari			
Db	2604	CGTTAATGAGATGCTGGGAGGCCAACAAAGGTCAACCCCATCCTCCAGGTGTTGGCA	2663	APPLICANT: Zyskind, Judith			
Qy				APPLICANT: Wall, Daniel			
Db				APPLICANT: Trawick, John			
Qy				APPLICANT: Carr, Grant			
Db				APPLICANT: Yamamoto, Robert			
Qy				APPLICANT: Forsyth, R.			
Db				APPLICANT: Xu, H.			
				TITLE OF INVENTION: Identification of Essential Genes in Microorganisms			
				FILE REFERENCE: ELTRA-034A			
				CURRENT APPLICATION NUMBER: US/10/282,122A			

;

;

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

;

Remaining Prior Application data removed - See File Wrapper or PALM.

;

NUMBER OF SEQ ID NOS: 78614

;

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 25766

LENGTH: 3381

TYPE: DNA

ORGANISM: Mycobacterium avium

US-10-282-122A-25766

Query Match 37.6%; Score 1361.6; DB 12; Length 3381;
 Best Local Similarity 63.2%; Pred. No. 0; Mismatches 1234; Indels 9; Gaps 2;
 Matches 2131; Conservative 0; Mismatches 1234; Indels 9; Gaps 2;

Qy	238	AAGATCTGGTAGCAAACCGGGGAATCCGGGTCCGGTTCGGGATCATTCCACCGCTAA 297	Db	298	ACCGGTGGCACGGTATTTACCCCGTGAAGATCGGGGATCATTCCACCGCTT 357	Db	70	CTGGAAATGGCCACCGGGGTGTATCCCTACGAGGAACGGCAATTGGTGCAACGGTTG 129	Qy	358	TTCGCTCTCTGAAGCTGTCCGATGGTACCGGAAGGCTACCCAGTCAAGGGTAACTGGAC 417	Db	130	AAGGCCGAGCTTACCAAGATGGTACGGGGCCACCCAGTGGTGAGGGCCATCTGTC 189	Qy	418	ATCGATGAATTATCGGTGGCAGCTAAAGTTAACCGATGCCATTACCGGATAC 477	Db	190	GTCGACGAGATGTCTGGCCTGGGGCTGGGGATGGCATCTACCGGCTAC 249	Qy	478	GGCTTCCTGCTGAATAATGCCAGCTTGGCCAGTGTGGGAAACGGCATACTTTT 537	Db	250	GGCTTCCTGTTGGAGAACCCGATCTGGGGGGCTGGGGCATCACGTTTC 309	Qy	538	ATTGGCCCACCCACAGGGTCTGTATCTCACCGGTGATAAGTCTGGGGTAACCGCC 597	Db	310	GTCGGCCCAGGGCGAGGTCTGGAGCTAACGGGATGGGCAAGTGGGGCATGGGG 369	Qy	598	GCGAAGAAGGGCTGGTCTGGCAGTTTGGGAATCCACCGGTAAAGTCTGGGGTAACCGG 657	Db	370	GCGGGGGCGGGCTTCGGGTGCTGGCCCTGCACCTGGGGAG 429	Qy	658	ATCGTTAAAGGGCTGAAGGGCAGACTTACCCATCTTGTGAAGGGCAGTTGGGGTGGT 717	Db	430	TTCGCTGAGGCCGCGGATGGGTTCCGGTCAAGGGGGTGGTCAAGGGGGGG 489	Qy	718	GGGGGACGGGATGGGGTTCCGGGATGGGGTATATGTCGAACCTGATGAGGCTTCG 777	Db	490	GGGGGGGGGATGGGGGGTCAACGGGATGGGGGGGGTGGGGGATGGGG 549	Qy	778	GCATCTGTAAGGTTGAAGGGCTGAAGGGGTTCCGGGATGGGGTATATGTCGAACCTG 837	Db	550	GCCAGCCGCTGAGGGGGTCCGGCTGGGACGCGCTGGTCTGGGGGGGGGG 609
----	-----	---	----	-----	---	----	----	---	----	-----	---	----	-----	---	----	-----	--	----	-----	--	----	-----	---	----	-----	--	----	-----	---	----	-----	---	----	-----	--	----	-----	--	----	-----	---	----	-----	--	----	-----	---	----	-----	---	----	-----	---	----	-----	---

QY 1918 TCCGTTGGAGCCACCTTACGATGGCGATGGCTTCCTCTGGAGAT 1977
 Db 1690 TCGGTGGAGTGGGGACTAACGACTGGGGCTCAAGGAGGAC 1749
 QY 1978 CCGTGGGACAGGCTCAGCAGGGATGCCAATGTAACATTCAAGTGCCTG 2037
 Db 1750 CCGTGGGAGGGTGAAGGGCTGAGGGATGCCAACATCTGCCTCAGATGCTG 1809
 QY 2038 CTTTCGGCGCGAACCCGTAACCCAGACTCCGCTTGCGGGCTTT 2097
 Db 1810 CTGGTGGGGTAACACCGTGGGTACAGCCCTATCCGGAGACGGCTTC 1869
 QY 2098 CTTAAGGAAGGCTGGGAGCATTTCAACCGGCTAAACGAC 2157
 Db 1870 GTCGGGAGGGGACCCGAGACGGATGGGACATCTGGCAAC 1929
 QY 2158 GTGGCTATGGCTTATTCGCACTTCGGGAGACCAACCCGGAG 2217
 Db 1930 GTGCACTGATGGCATGGCAATCTGGGATCCGGCATAGCGAAC 1989
 QY 2218 TACTACCTAAAGATGGCAGAGGAACTGGTCAAGTCAAATGAAAAGCTCTAACCCCTGGAT 2277
 Db 1990 GTGGCGATGTCTTAACCCGGGACCTGGGAGGGCATAGCGGA 2049
 QY 2278 TACTACCTAAAGATGGCAGAGGAACTGGTCAAGTCAAATGAAAAGCTCTAACCCCTGGAT 2337
 Db 2050 TATTACCTGAAGGTGGCGACCAAGATGGTGAAGGTTAACGGTGGAC 2109
 QY 2338 GATAATGGCTGGTCTGGCCAGTGGTAACCGTGGTCAACGGCACTGGCGT 2397
 Db 2110 GACATGGCCGGCCCTGGCTGGGCAACGGGGGACCTGGTCAAGTGGTCAAGTGGTCAACGGTGGCGT 2169
 QY 2398 GAATTGCACTTGCCAGTGGCACGGTCAACCCACGACACTGGCAACC 2457
 Db 2170 CGGTTCGACCTGGGGTGCACGGTGCACACCCTGACACGGGGGGGAGACGGTGGGAC 2229
 QY 2458 TACTTGGCTGAGCTCAAGCTGGTGCAGATGCTGGTGCAGGGTGGCTGGGCAACCACTGTCT 2517
 Db 2230 TAGTGGGGCCCTGGCAAGCCAGTGGCTGGGCAATGGTGTGCACTGGGCAACGGGCTCGCC 2289
 QY 2518 GGCACCACTCCAGCATCCCTGCAAGCTGGTGCATTGGTGTGCACTGGGCAACCCGTGCG 2577
 Db 2290 GAAACCACAGCCAGCGGCACTATGTCGATCGTGGCCGAAACACGGAGAT 2349
 QY 2578 GATAACGGTTTGGCCTCGAGGCTGTTCTGACCTCGAGCCGTACTGGAAAGCACTGGC 2637
 Db 2350 GACACGGGTTGTCCTGGGGGGTGTGCGATCTGGAGGGCTACTGGAGGGCTGGGA 2409
 QY 2638 GGACTGTACCTGCCATTGAGTCTGGAAACCCAGGGCACTGGCTTACGCCAC 2697
 Db 2410 AAGGTATACTGGTCCTTCGAATCCGGTCTTCGGGGGGTGTACCCAC 2469
 QY 2698 GAAATCCCAGGAGCAACTACGAGCCACCTGGCAAGGGCACTGGGCTTGCG 2757
 Db 2470 GAGATCCGGCCAAATTGTCGAATCTGTCAGGGGATTGGCTGGCG 2529
 QY 2758 GATCGTTTGGAACTCATCGAAGACAACCTGGCAACGGCTTAATGAGATGCTGGGACGCCA 2817
 Db 2530 GACCGGTTGGAGCATCGAAAAGCCCTACGCCGGCGGACGCGATTGGGACACCTG 2589
 QY 2818 ACCAAGGTACCCCATCTCAAGGGTGTGGCGACTCCACCTGGCAAGGGCACTGGCTGGCG 2877
 Db 2590 GTCAAGGTACACCGTCCAGZAACTGGCTGGGCACTCCGGCTGGGCG 2649
 QY 2878 GGTGGGATCCAGGAGACTTGGTGGCCGATCACAAGATGACACTGGCTGGGCG 2937
 Db 2650 GGTGGGGGGCAGGACTTCGCGGAAGACCCCTCCGGTACGACATCCGGATTGGT 2709
 QY 2938 ATCGGTTCTGGCGGAGACTTGGTAACCTCCAGGTGGCTGGCGAGGCCACTGGC 2997
 Db 2710 ATGGCTTCTGGGGAGCTGGTGGCGGAAGCCGGGGTGGCTGGCG 2769
 QY 2998 ACCCGGGCACTGGAAAGGGCAACCTCTGACGGAAAGTCCCTGAGGAA 3057

RESULT 8
 US-10-282-122A-28626
 Sequence 2B626, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 | APPLICANT: Wang, Liangsu
 | APPLICANT: Zamudio, Carlos
 | APPLICANT: Malone, Cherry
 | APPLICANT: Haselbeck, Robert
 | APPLICANT: Ohlisen, Kari
 | APPLICANT: Zyskind, Judith
 | APPLICANT: Wall, Daniel
 | APPLICANT: Trawick, John
 | APPLICANT: Carr, Grant
 | APPLICANT: Yamamoto, Robert
 | APPLICANT: Forsyth, R.
 | APPLICANT: Xu, H.
 | TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 | FILE REFERENCE: ELTRA-034A
 | CURRENT APPLICATION NUMBER: US/10/282,122A
 | PRIOR APPLICATION NUMBER: 2003-02-20
 | PRIOR FILING DATE: 2000-03-21
 | PRIOR APPLICATION NUMBER: 60/191,078
 | PRIOR FILING DATE: 2000-05-26
 | PRIOR APPLICATION NUMBER: 60/206,848
 | PRIOR FILING DATE: 2000-05-23
 | PRIOR APPLICATION NUMBER: 60/207,727
 | PRIOR FILING DATE: 2000-05-26
 | PRIOR APPLICATION NUMBER: 60/230,335
 | PRIOR FILING DATE: 2000-09-06

```

; PRIORITY APPLICATION NUMBER: 60/230,347
; PRIORITY FILING DATE: 2000-09-09
; PRIORITY APPLICATION NUMBER: 60/242,578
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 60/253,625
; PRIORITY FILING DATE: 2000-11-27
; PRIORITY APPLICATION NUMBER: 60/257,931
; PRIORITY FILING DATE: 2000-12-22
; PRIORITY APPLICATION NUMBER: 60/267,636
; PRIORITY FILING DATE: 2001-02-09
; PRIORITY APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28626
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-10-282-112A-28626

Query Match          35.7%; Score 1294.4; DB 12; Length 3384;
Best Local Similarity 62.0%; Pred. No. 0;
Matches 2099; Conservative 0; Mismatches 1276; Indels 9; Gaps 0

Qy          238 AAGATCTTGTAGCAAACGGCGAAATCGGGTCCGTGCTTCCGTGCTGCAGCACTCGA
Db          10 AAGGTGCTCGCCAATCGGGAGATCGCGATTCGGCCTTTCGTGCCCTACGAA

Qy          298 ACCGGTGCACGGTAGGTATTACCCCCGGTAAGATCGGGATCATTTCCACCGCTC
Db          70 CTGGCGTGGAACCGTGGCGTTATCCGTACGAGGACCGAATTGCAGCACCGTCT

Qy          358 TTTGCTTCTGAAGGCTGTCCGATTGGTACCCGAAAGGCTCACCAAGGCTAACCTGG
Db          130 AAGGGGACGGACTTACCGATCGGGACATCGGTACCCGGTGCATGCATACTGTGTC

Qy          418 ATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCGGGATA
Db          190 GTGGACGAGATCGTGGACGGCCCCTGGGATCTGGCTGGGCAATGGGGCATCGCTTGGCTA

Qy          478 GGCTTCCTGTGAAATGCCAGGTTCTGGATCTGGGTGCGAGTGTGGAAAACGGCATTA
Db          250 GGGTTTCTATGGAGAATCCGGATCTGGCTGGGCAATGGGGGGCATCGCTTGGCTA

Qy          538 ATTGGCCAACCCCAAGGGTCTGGTGTCAACGGGTGATAAGTCTGGGGGGTAAACGGC
Db          310 GTGGTCCAGGCCGAAGTGCTGGAGCTGGGAATAAGTCTGGCCATCGGGCATCGGGC

Qy          598 GCGAAGGAAGGGCTGGTGTGGCAAGGGCTGGGAATCCACCCGAGCAAAAACATCGATG
Db          370 GCCGGAAAGCCGGCTGGCGTGTGATGTCTGGGGCTCGGGCATCGGGCATCGGGC

Qy          658 ATCGTTAAAAGGGCTGAAGGCCAGACATTACCCCATCTTGTGAAGGCCAGTTGGGGT
Db          430 CTGGCTGTGGTTGGGGCATGCCGTTTCGTTGTCAAAGGCCAGTTGGGGT

Qy          718 GGCGGACGGGTATCGGTTGTGCTTCACTGAGCTTGGGATCCTTGGGATCTGGAAACAGG
Db          490 GGGGGGGGTATGGGTGCGGCGATATCGGGGGCTCCGGAGGGATCGAAGG

Qy          778 GCATCTCGTGAAGGCTGAAGGGCTTTCGGGATGGGGGTATATGTCGAACGGTGTCTG
Db          550 GCCAGCGGGAAAGCCGAGTCGGGTCTGGGACGGCTATCTCGAGGCGAGT

Qy          838 ATTAACCTCAGGATATTGAAGTGCAGATCCTTGGGATCACACTGGAGAAGTTGTAC
Db          610 ATCAATCCAGGCCACATCGAGGTGCAGATTCTGGGACAAACTCGGGGACGGTATCCP

Qy          898 CTTTATGAACGTTGACTTGCAAGCTCACTGGCGTGTCTGGAAAAAGTTGTGAAATGGCC
Db          670 CTCTATGAGCGTGTGACTGCAGGTGTGACTGCAGGTGCTGGGACATCGAGGTATCGAGGCTGGGG

```

QY	958	GCACAGCATTGGATCCAGAACTCCAGAATTCGCTGATCGGTGATTGGCATTTCGCAATTGGGATGGTAAAGTCTCTGC	1017
Db	730	GGCCGCACCTGGCGGTGCGGACTGCGGTACAAGATGTCGCTCGATGGCTTGCGCTCGCC	789
QY	1018	CGCTCCATTGGTTACCGGGGAACCGTGAATTCTTGGTCGATGAAAAGGGCAAC	1077
Db	790	CGCCATACTGGTACAGTCAGCTGGCACCCGGTCAAGATGTCGCTCGATGGCTCGCTCGCC	849
QY	1078	CACGTCTTCATCGAAATGAAACCCACGTATCCAGGTTGAGCACACCGTGAACCTGAAGAAGTC	1137
Db	850	TATGTCCTCATCGAGATGAATCCGGGGTTCAGGTGGAGCACACGGTACCGAGGAGATT	909
QY	1138	ACCGAGGGACCTGGTAAGGGCAGATGGCAGTTGGTGCACCTTGAAAGGAA	1197
Db	910	ACCGACGTCGACCTGGTGGCAAGCCACGGCACTACAGTGCCGGATCGAACAA	969
QY	1198	TGGGTCTGACCCAAGATAAGATCAAGAACCCACGGTGCAGGCACTGCCGATTCACC	1257
Db	970	TGGGCTGCGGAGGACATCGCACCGCATGGGGCAACTACAGTGCCGGATCAC	1029
QY	1258	ACGGAAGATCCAAACAAACGGCTTCGGCCAGATAACGGAACTATCACCGGTACCGCTCA	1317
Db	1030	ACCGAGGATCCGGCAACGGCTTCGGCCAGGACACGGGGATCAGGGTGGCAC	1089
QY	1318	CCAGGGAGCTGGCTTCGTCGTTGACGGCTCAGGCTCGGTGGCGAAATCACCGCA	1377
Db	1090	GCGGGGGTGGCGGTCCGGTCAAGCTGGGAAACCTGGGGATCAGGGTGGCAC	1149
QY	1378	CACTTGAECTCCATGCTGGTGAATAATGACCCCTGCCGTGGTTCGGACTTTGAAACTGCTGTT	1437
Db	1150	TACTTCGAETCCATGCTGGTCAAGCTGACCTGGGGCGGTACCTCCCTACCGCAGTG	1209
QY	1438	GCTCGTGACAGGGCGTTGGCTGAGTTCACCCGTTGTCAACCAACATTGGT	1497
Db	1210	AGCCGTGGCGGGGATCGGGAGTTCCGGACTTCCGAGGGGTATCGACGAATAATTCCG	1269
QY	1498	TTCTTGCGTGGCTGGGAAAGGGACCTTCAACTTCCAAGGGCATCGCCACCGGATTC	1557
Db	1270	TTCTGCAAGGGTCCGGATGACCCGGACTTCCGAGGGGGTCAACACGTCCCTTC	1329
QY	1558	ATTGCCATCACCGCACCTCCACCTCAGGCTCACTGGCTGATGAGCAGGACGCATC	1617
Db	1330	ATTGATGAGGGCGGGATCGGGAGCTTCCGGGATCCGGGCTCGGGCACCAAGATC	1389
QY	1618	CTGGATTACTGGCAGATGTCACCGTGAACAAGCCTCATGGGTGCGTCCAAAGGATGTT	1677
Db	1390	CTTAACCTCCTGGCGATGTCACCGTCAACAACCCGTATGGCTCGGTCAACGATC	1449
QY	1678	GCAGGCTCCTATGGATAAGCTGGCTTAACATCAAGGATCTGCCACTGCCACCGGGTCCCGT	1737
Db	1450	TACCCGGACAGCTGGCGATCTTGATCTGGGGCCACCAACGGGTCCAAAG	1509
QY	1738	GACCGCCTGAAGGAGCTTGGCCAGGCCACCTGGCTGATCTCCGTGAGGACGCA	1797
Db	1510	CAGCGACTAGTCAGGTTGGGGATGGGAAGGATTTCGTTGGCTGGGGAGTGGCTACCCGAGTA	1569
QY	1798	CTGGCAGTTACTGATAACACCTTCCGGATGGCACCCAGTCCTTGCGACCCGAGTC	1857
Db	1570	TCGGGGTACCGGATAACACATTCGGGATGCTACCCGAGTGGCTACCCGAGTA	1629
QY	1858	CGCTCATTCGCACTGAAGCCTGGGGCAGAGGGCGTGCACAAAGCTGACTCCTGAGCTTTGAGGAT	1977
Db	1630	CGCACCGGGGACTGTCGGGGTGGCACCGTATCTGGGGACATGCCGAGCTGGTTG	1689
QY	1918	TCCGTTGGCAGGGCTCGACGGGCTGGCCAGGGCGTGCACAAAGCTGACTCCTGAGCTTTGAGGAT	1977
Db	1690	TCCGTTGGAGTGTGGGGGTGGGACTTACGATGTCGGCTTCTCAAGGGAGAT	1749
QY	1978	CCGTGGGACAGGCTCGACGGGCTGGCCAGGGCGTGCACAAAGCTGACTCCTGAGCTGGTTG	2037
Db	1750	CCCTGGGAACGGGTGGCACACTGGGCAATGCCAATATCTGCTTGGCAGATGCTA	1809
QY	2038	CTTCGGGGCGAACACCGTGGGATAACACCCGGTACCCAGACTCCGACTCCTGCTGGCGGTT	2097

Db	1810	TGGGGGGCGCAATTACCGTGGCTAACGGCGTAACGGTGGCGTTAACGGGAAATCGTGACGTGGCGTT 1869	Db	2884	TTATTCCCAGTCCAACAAAAGGAATTCAAATGAGGAACCGGAAACGGCTAACGGGAAAGGCCAACGGTCG 2943
Qy	2098	GTTAAGGAAGCTGCCAGCTCGGGTGGACATCTTCGGAATCTTCGACCGCCTTAACGGAC 2157	Qy	3178	GCGCTGGATGATGTCGAAATTCTTACGGCTTACGGCTGGAGACTTTGATCCGC 3237
Db	1870	GTGCGAAGAACGCCAACGGTATCGACATCTTCGATCTTCGACGCTCAACAAAC 1929	Db	2944	CAATTGTCGGCCAACCAAGGTTCTTCGATCTTCGACGCTCAAGGATGGTGAAG 3003
Qy	2158	GTCTCCAGATGCGTCAGCAATCGCAACGGTAGCTGGAGACCAACCCGGTAGCCGAG 2217	Qy	3238	CTGCCAGATGTCGGCACCCCACTGCTTCTGGATGGCATCTGAGGCCAGACGAT 3297
Db	1930	ATCGAGTCATGGTCGGCGATCGCAAGTACGGAAACAGGTTCTGCGATAGCGAA 1989	Db	3004	CTG---GAGCTGGGGTAGCTGGATCGGGGATGGGCAATTCCGAACCGGACGAA 3060
Qy	2218	GGGCTATGGCTTATTCTGGTATCTCTGATCCAATGAAAAGCTCATACCTGGAT 2277	Qy	3298	AAGGGTATGCCAATGTCGGCCAAACGTCAACGCCAGATCGGCCAATGCGCC 3357
Db	1990	GTGCGATGCTAACGGGACCTAACGGGACTTACCGATCGGGTAACAGCTGGAC 2049	Db	3061	CGCGCATGCGAACGGTATGTCATCTAACGGCAGCTGGCTAGTGC 3120
Qy	2278	TACTACCTAAAGATGGCAGGGAGATGGTCAAGTCTGGCTCACATCTGGCCATTAA 2337	Qy	3358	GACCGCTCCGTTGAGTCTGTCACCGCAACGGCAGAAAGGAGATTCTCCAACAGGGC 3417
Db	2050	TACTACCTGAAACTGGTGTGAGCAATCGGGCCATGTGCTGGGATCAAG 2109	Db	3121	GACCGCAGGATTGCCAGTGGCTTCGGCCGAGAAAGGGCAATCCCGGA 3180
Qy	2338	GATATGGCTGGTCTGCCAACGCTGGTAACCAAGCTGGTCAACGGCACTGGCGT 2397	Qy	3418	CATGTTGCTGCCACCATTGGCTGGTGTCAACCGTGACTGTTGCTGAAAGGTGATGAGGTC 3477
Db	2110	GATATGGCTGGACTGTGCCCCGGCTCAAAGGTGGTCAGGCGCCATGTGCTGGGAGTCAAG 2169	Db	3181	CACATGCCGGCATTTGGGAGTGTCAAGGGTGGGTGTGCGTGGGGGTC 3240
Qy	2398	GAATTGATCTGCCAGTGCACGTGCACTGCCAACGACACTGGGGTGGCAACC 2457	Qy	3478	AAGGGTGGAGATGCACTGGGCTATGAGATGCAAGAACAAATCACTGCT 3537
Db	2170	CGCTTGACCTGCCGGTCAACCTGCAACCCCAGACACTGGGGTGGCACTGGCGAC 2229	Db	3241	GGCGCGGCCAACCATGCCACCATGCCACCATGAGGGATGAAGATGGAAGGCCGATCACGCC 3300
Qy	2458	TACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTTGGTCACTGGACCAC 2517	Qy	3538	TCTGTTGACGGAAAAATCGATCGGTTCTGCTGCAACGAAGGTGGAACGGGGC 3597
Db	2230	TATGGCCGGTTRGGACGCCATCCCTGTGCCATTGGTGCCTGGCATGGCGCC 2289	Db	3301	CCGGTGGGACCGTGGGGACACCCGGGATGGGGGGGGGGGGGGGGGGGGGG 3360
Qy	2518	GGCACCACTCCCAGCAGCTCCCTGTGCCATTGGTGCCTGGCATGGCGCC 2577	Qy	3598	GACTTGATGTCGTTCTGCTGTTCTAA 3621
Db	2290	GGAACGACCGCCAGGCCAACGGCGTGAAGCTGCTGGCGCTGCCAACCGAGTAC 2349	Db	3361	GACCTGTTGGTGGTGGGGATGCTGA 3384
RESULT 9					
US-10-282-122A-26500					
; Sequence 26500, Application US/10282122A					
; Publication No. US20040029129A1					
GENERAL INFORMATION:					
; APPLICANT: Wang, Liangsuo					
; APPLICANT: Zamudio, Carlos					
; APPLICANT: Malonne, Cherry					
; APPLICANT: Haselbeck, Robert					
; APPLICANT: Ohlson, Kari					
; APPLICANT: Zyskind, Judith					
; APPLICANT: Wall, Daniel					
; APPLICANT: Trawick, John					
; APPLICANT: Carr, Grant					
; APPLICANT: Yamamoto, Robert					
; APPLICANT: Forsyth, R.					
; APPLICANT: Xu, H.					
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms					
FILE REFERENCE: ELITRA_034A					
CURRENT APPLICATION NUMBER: US/10/282,122A					
; CURRENT FILING DATE: 2003-02-20					
; PRIOR APPLICATION NUMBER: 60/191,078					
; PRIOR FILING DATE: 2000-03-21					
; PRIOR APPLICATION NUMBER: 60/206,848					
; PRIOR FILING DATE: 2000-05-23					
; PRIOR APPLICATION NUMBER: 60/207,727					
; PRIOR FILING DATE: 2000-05-26					
; PRIOR APPLICATION NUMBER: 60/230,335					
; PRIOR FILING DATE: 2000-10-23					
; PRIOR APPLICATION NUMBER: 60/253,625					
; PRIOR FILING DATE: 2000-11-27					
; PRIOR APPLICATION NUMBER: 60/257,931					
; PRIOR FILING DATE: 2000-12-22					
; PRIOR APPLICATION NUMBER: 60/267,636					

; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 26500
 ; LENGTH: 3381
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium bovis
 ; US-10-282-122A-26500

	Query Match	Score 1292.2;	DB 12;	Length 3381;
;	Best Local Similarity	62.0%;	Pred. No. 0;	
;	Matches 2095;	Conservative	0; Mismatches 1273; Indels 9;	Gap
Qy	238 AAGATCTTGGTAGCAAACCGGGGAAATCGGGGTCCGTGCCTTCCGGACTCTG			
Db	10 AAGGTGCTCGTCAATCGGGGAGATCGGGATCGGGCTACGGCTACGGTCA			
Qy	298 ACCGGTGCAGCCACGGTAGCTATTACCCCCGTGAAGATCGGGATCATTCCACCGCT			
Db	70 CTGGGGTCTCGGAACCGTGGCGTTATCCGTACGGAGCACCGAATTTCGAGCACCGTC			
Qy	358 TTRGCTTCCTGAAGCTGTCCGCATTGGTACCGAAGGGCTCACCAAGTCAAGGGTACCTGG			
Db	130 AAGGGGGACGAGTCTTACCAAGATCGGGGACATCGGTCAACCGGTGCAATGCCATCTGT			
Qy	418 ATCGATGAAATTATCGGTGCAGCTAAAAAGTTAAAGCAGATGCCATTACCCGGGAT			
Db	190 GTCGACGGAGATCGTGCAGCGGCCGTCGGGGACTACCGCTATCTACCTGGCT			
Qy	478 GGCTTCCTGTCTGAAAATGCCAGGCTTGCCTGATCTCAACGGGTAAAGGCAATTACTT			
Db	250 GGGTTCTATCGGAAATCGGATCTGGCTGGGATCGGGCATCGCTAGCT			
Qy	538 ATTGGCCAACCCCAGAGGTCCTGATCTCAACGGGTGATAAGTCTCGGGTAACCC			
Db	310 GTCGGTCCAGGGCGAACGGTGCCTGAGCTGGGAATAAGTCTCGGCCATCGGCC			
Qy	598 GCGAAGGAAGGGCTCTGCAGTTTGCGGAATCCACCCGAGCAAAACATCGATC			
Db	370 GCCCGGGAAGCCGGCTTGCCCGTGCATGTCCTCGGGCCTCGGTGACCG			
Qy	658 ATCGTTAAAGGCCCTGAAGGCCAGACTTACCCATCTTGTGAAGGCAGTTGCCGGT			
Db	430 CTGCTGTCGGTTGGCGGCCATGCCGTTGCTCACCTGATGAGCTCGCAAATTAGCAACAC			
Qy	718 GGGGGACGGGTATGGGTTGGTGCCTCACCTGATGAGCTCGCAAATTAGCAACAC			
Db	490 GGGGGGGGTATGGCTCGTGCATGCGGATATCGGGGCTTCGGAGGCATCGAACAC			
Qy	778 GCATCTCGTGAAGGCTTGGCGATGGGGTATATGTCGAACGTTGCT			
Db	550 GCCAGGGAAAGCCGAGTCGGGTTGGGGACCGGTTCTGGGACGGTCTATCTCGAGCAGGCCAC			
Qy	838 ATAACCCCTCAGCATATTGAAGTGCAGATCCTGGCGATCACACTGGAGAAGTTGTA			
Db	610 ATCAATCCACGCCACATCGAGGTGCAGATTCTGGGACAACCTCGGGGACAA			
Qy	898 CTTATGAAACGTGACTGCTCACTGCAGGGTCTGGTCAACCAAAAGTTGCGAAATTGCG			
Db	670 CTCTATGAGCGTGAATGCGGTCTGGCTACAGATGCGCTCGCCATCAGAAGGTCA			
Qy	958 GCACAGGCAATTGGGATCCAGAAACTGCGTGAATCGCATTTGCGGATGGCAGTAAGTTCT			
Db	730 CGCCGGCACCTGGGAGGTGGCTTACAAGATGCGCTCGGATGGCTGGCTTC			
Qy	1018 CGCTCCATTGGTACAGCTGGGACCCGTGAATTCTGGTCAATGAAAGGGCA			
Db	790 CGCCATATCGGGTACAGCTGGCAGGGCACCGTGGCTTCTGGAGGCGAGCCGAGGGCA			
Qy	1078 CACGTCCTCATCGAAATGAAACCCACCGTATCCAGGTGAGGCCACACCGTGAAGAAAC			

RESULT 10
 US-09-917-800A-1566
 Sequence 1566, Application US/09917800A
 Patent No. US20020119462A1
 GENERAL INFORMATION:
 APPLICANT: Mendrick, Donna
 APPLICANT: Porter, Mark
 APPLICANT: Johnson, Kory
 APPLICANT: Castle, Arthur
 APPLICANT: Blashoff, Michael
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917,800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,880
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/290,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/290,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/292,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: PatentIn Ver. 2.1
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012744
 Query Match 18.8%; Score 681; DB 9; Length 3945;
 Best Local Similarity 54.2%; Pred. No. 3.2e-197;
 Matches 1521; Conservative 0; Missmatches 1260; Indels 24; Gaps 6;
 US-09-917-800A-1566

2301 TCAGCTCCCTCCGGACCGGTTCCCCGACCTCCCACTGCACATCCATACCCATGACACAT 2360
 2438 CGGGTGGCAGCTGGCAACCTACTTTGCTGCAGCTCAAGCTGGTGCAGATGCTGTGACG 2497
 2361 CAGGGTCAGGTGGCAGCCATGGCCTGTGACAAGCTGGGCTGATGRTGTGGATG 2420
 2498 GTGCTTCCGCCAACCTCTGGCACCCTCCCAAGCATCCCTGCTGCCATTGTCATTGCTG 2557
 2421 TGGCAGTCAGCTCATGTCTGGATGACCTCACAGGCCAGCATGGGGCTGTTGACTACAGTG 2480
 2558 CATTTCGGCACACCCGGTACCGGTTGAGCCCTGGGACTACGGCTGTTCTGACCTCGAGC 2617
 2481 GTACCAAAGGGACTCCTCTGGACACAGGGTACCCCTGGAGGGTGTGTTGACTACAGTG 2540
 2618 CGTACTGGAAAGGCACTGGCGGACTGTACCTGTCATTGA-----GTCTGGAACCCCAG 2671
 2541 AGTATTGGAAAGGGCTCGGGGCTGTATGGAGCCCTTGTGATTGCAACGGCTTACCATGAAGT 2600
 2672 GCCCACCCGGTGGCTTACCGCCACGAAATCCAGGGACAGTTGTCACCTGGGTG 2731
 2601 CTGGCAACTCAGCTGTGTTATGAGAATGAGGATCAGGGCCAGTACACCAACCTACACT 2660
 2732 CACAGGCCACGGCACTGGCCTTGGGATCGTTCGAACTCATCGAAGACAACCTACGGAG 2791
 2661 TCCAGGCCACAGGACTTGGCTCCAAGTCAAGGAGGTCAAGAAGGCTATGTGG 2720
 2792 CCGTTAATGAGATGGGACCCAAACCAAGGTCACCCCATCCTCCAAGGGTTGGCG 2851
 2721 AGGCTAACAGGATGGCTGGGACCTCATCAAGGTGACACCATCCTCCAAGATGTGGGG 2780
 2852 ACCTCGCACTCCACCTGGGGTGGGATCCAGCAGACTTGGCTGCCGATCCAC 2911
 2781 ATCTGGCCAGTTCATGGTGCAGAACGGGTTGAGCCGGCAGAGGTCAAGGCTAGGG 2840
 2912 AAAAGTACGACATCCCAAGACTCTGTCACTCGCGTTCTGGTAACCCCTC 2971
 2841 AAGAGCTGTCCTTCCCCGCTCTGGGAGTTCTGAGGGCTACATTGGCATTCCTCC 2900
 2972 CAGGTGGCTGGCCAGAGGCCACTGGCACCCGGCAACTGGGAAGGCC 3016
 2901 ATGGGGTTTCCCTGAAACCCCTTAAGGTGCTAAAGGACC 2945

RESULT 11

US-09-880-107-3029

Sequence 3029, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3029

LENGTH: 4017

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 S72370

US-09-880-107-3029

Query Match 18.7%; Score 677.4; DB 9; Length 4017;
 Best Local Similarity 54.4%; Pred. No. 4.1e-196;
 Matches 1525; Conservative 0; Mismatches 1256; Indels 24; Gaps 7;

233	TCAA	AAAGATCTTGGTAGGCAAACCGGGGAAATC	GGGTCCGGTCAAGGCAGC	292
192	TCA	AGAAAGTCATGGTGGCCAACAGAGGTGAGATTGCCA	TCCGGTCTGGTGGCTGCA	251
293	TCGAA	ACCGGTGAGCCACGGTAGCTATTACCCCCGTGAAGATCGGGGATCATTC	CACC	352
252	CGGAGCTGGC	ATCCGACCGTAGCCATCTACTCTGAGCAGGACACGGGCAAGATGGCACC	311	
353	GCTCTTTGCTTCTGAAAGGCTGTCGGCAT	TGGTACCCAGGCTACCCAGTCAAGGGTACCC	412	
312	GGCAGAAAGCAGATGAAGGCCTATCTCATGGCCCCTGGCTGAGGGCTAAC	CC	371	
413	TGGACATCGATGAAATTATCGGTTGCAGCTAAA	AAGCTTAAGCAGATGCCATTACCCGG	472	
372	TGGCACATCCCAGACATCATCAAGGTGGCCAAGGAGAACAAACGTA	GATGCA	GTGCCACCCCTG	431
473	GATA	CGGGCTTCCCTGCTGAAATGCCAACGGGAAACGGCATTAA	GGGTGCGGAGCTTG	532
432	GCTACGGGTTCCCTCTCTGAGCGGGACTTC	GGGCTGGCAGGATGGCTCC	491	
533	CTTTTATTGGCCAACCCCAGAGGGTCTTGATCTCACCGGTGATAAGTCTCG	GGCGGTAA	592	
492	GGTTTATTGGTCCAAGGCCAGAAGTGGTCCGCAAGATGGGAGACAAGGTGG	GGCCGGGG	551	
593	CGGCCGGAAGAAGGGCTGGCTGCCAGTTTGGGG--	-AATCCACCCCGAGCAAACAA	649	
552	CCATGCCATTGCTGCCGTGTTCCCGTGGCACAGATGCCCATCAC	GGGGCTCC	611	
650	TCGATGAGATCGTTAAAAGGGCTGAAGGCCAGACTTACCCC	ATCTGAGCTTCCCATCATCTTC	AAGGGGCT	709
612	TGCATGGCCCACGGAGTTCTCCAAACACTACGGCTTCCC	ATCAAGGGGCT	671	
710	CCGGTGGTGGCGGACGCCGTTATGCCATTGAGCTTCCGAATTAG	TTGTGAAGGGCAGTGT	769	
672	ATGGGGTGGGGGGCGTGGCATGAGGGTGGCACAGCTACGAGGAGCTG	GGGAGAGAATT	731	
770	CAACAGAAGCATCTCGTGAAGGCTGAAGGGCTTTCGGCATGGGGTATATG	TGGGAAAC	829	
732	ACACCCGGCCTACTCAGAGGGCCTGGCCACATCGAGGTGCA	GGGCTTGGGAATGGGGCT	791	
830	GTGCTGTTGATTAAACCTCAGCATTGAAAGTGCAGATCCTGGGATCAC	ACTGGAGAAG	889	
792	AGTTCATCGAGAACGCCACGGCACATCGAGGTGCA	GATCTGGGACGACTATGGGA	851	
890	TTGTACACCTTATGAACCGTGACTGCTCACTGCAGCGTCGT	CACCAAAAGTTGTG	949	
852	TCCTGCACCTGTACGAGGACTGCTCCATCCAGGGCACCCG	GGGACTCGGCT	911	
950	TTGGCCAGCACGGATTGGATCCAGAACTGGCATTTGTGGGAT	TGGGATGCGAGTAA	1009	
912	TTGGCCGCCACCTGGACCTGGGAGACTCGGCTCACCGGACTCTGTGA	TGGGACTCGGCT	971	
1010	AGTTCTGGCTCCATTGGTACCGGGGAACTTCTTGTG	GGGATGCGAAA	1069	
972	AACTCGCTAAACAGGGGGTACGAGAACGGCAGGG	GGGACAGGG	1031	
1070	AGGGCAACCACGTCTTCATCGAAATGAACTCCAGGTATCC	CAGTTGAGCACACCGT	1129	
1032	ACGGCAAGGCAACTTCTCGAGGTCA	CTCCGGCTGAGATCCACGGT	1091	
1130	AAGAAGTCACCGAGGTGGGACCTGGTGAAGGGCAGATGGC	GTGGCTGGCAACCT	1189	
1092	AGGAGATCACGGACGCTAGACCTGGTCCATGCTCAGATCC	GGGTGGCTGAGGACACGGT	1151	
1190	TGAAGGAATTGGGTCTGACCCAGGAAAGATAAGATCAAGAC	CCACGGTCACTGCAGT	1249	
1152	TACCGACCTGGGCTGCCAGGAGAACATCCGCATCAACGGG	GGGACACGGGCC	1211	
1250	GCATCACCACGGAAAGATCCAAACAAACG	GGCTCCGGCAGATAACGGAAACTATCACCGCGT	1309	
1212	GGGTCAACCACGGGACCCGGCCACGTTCCAGGCC	GGGACACGGGACACGGGCC	1271	

	1	AAGATCCTCATGCCAACGGTAGCTGATCGCCATCCGGTGAAGTCGGCAACGGGAAACGGGCTATGGCATCGGGCATGGGCAACGGAG 60	Db	1081	GCCTATCGCTGCCAACGGCACACTTGAATGCCATGGCATCGGGCATGGGCAACGGGCTATGGCATCGGG 1140
QY	298	ACGGTGCAGCCACGGCTATTTACCCCCGTAAAGATCGGGGATCATCCACCGCTCT 357	Qy	1363	GGGAAATCACGGCACACTTGAATGCCATGGCATGGGAAACGGGCTATGGCATCGGGCATGGGCAACGGGCTATGGCATCGGG 1422
Db	61	ATGGCAAGAGACGGTGCCTATGCCGGTCTATGCCGGAAAGACAAGCTCGTCCACCGCTTC 120	Db	1141	GGGTCACTCACCCGCTATTACGTTCACTCCCTCGTGAAGGTCAAGGGCTGGCTGAGTTCAACCGTGCTGGTGT 1482
QY	358	TTGCTCTGAAGCTGGCATGGTACCAAGGTCAAGGTGACCTGGAC 417	Qy	1423	TTRGAAACTGCTGGTGCACACGGCGGTGGCTGAGTTCAACCGTGCTGGTGT 1260
Db	121	AAGGGGACGAGGCTACGGATGGGCTCTGGCGAGGGCTATCTCTCG 180	Db	1201	CCCGAAAAGGCCATCGGCCATGGACCGGGATGGCATGGGAGTTCCGATTCGGCATCGGGCTGG 1320
QY	418	ATCGTGAATTATCGTGCAGTTAAAGCAAGATGCCATTACCGGGATAAC 477	Qy	1483	GCAACAAATGGGTTCTGCTGGGAAGAGGAACCTTCACTTCCAAGGCC 1542
Db	181	ATCCCCGAGATCATCCGGATCGTGGGGCGAGATGTCGGATGCCATCCACCGCTAC 240	Db	1261	GCCAAACATCGCCTTCGTCGAGAAACCTGCTGAAGCACCGGAGTTCCGACTATTC 1380
QY	478	GGCTCTGTTGTAATGGCCAGCTTGCCAGTGTGGAAACGGCATTT 537	Qy	1543	ATGCCAACCGGAACTGGGTTCTGGCATACCCGACCTTCAGGCTCCACCTGCTGATGAT 1602
Db	241	GGGTTCTGTCGAGAAACCCGATTTCTGTCAGGGCTCGGACGGGGCATGCCCT 300	Db	1321	TACAGGAGAAATTCTGACAGGCCGACCTTCACCGTAAACTCAAGCGTGGAC 1656
QY	538	ATTEGCCCACCCAGGGTTCTGATCTCACCGGTGATAAGTCTCGCCGGAAACGGCATTT 537	Qy	1603	GAGCAGGGACGAACTTGGATTACTTGGAGATGTCACCGTGTAACAGGCTC-----AT 1656
Db	301	ATCGGCCAGAGGCGAGACGGCTCGGGGAGATGCGGGCTCGGACGAGGGCATGGGTG 360	Db	1381	CGGGGAGAAGATCCGACCTACCGTAACTCAAGGGGAAACCCGAGAGCG 1440
QY	598	GCGAAGAAAGGGCTGGTCTGCCAGTTGGGAATTCACCGGAAACCATCGAT 654	Qy	1657	GGTGTGGTCCAAAGGATGGTGCAGCTCCCTATGATAAGCTGCTTAACATCAAGGATCTG 1716
Db	361	GCCATGGCCGGGGGATCCCGGATCGTGGGCTCGGACGAGGGCTCGGGCG 420	Db	1441	GCACGGGGTCCGGCCACCTCGGACATCGGACGAGGGCAACCCGAGGG 1500
QY	655	GAGATCGTTAAAGGCGTGAAGGGCAGACTAACCCCATCTTGTGAAGGGCAGTGGCG 714	Qy	1717	CCACTGCCACGGGTTCCCGTGACCCGCTGAAGGAGCTTGGCTTGGCTG 1776
Db	421	GAGATCAAAGGGCAGGGGGAGATCGGCTATCGGCTCAAGGGCTCGGG 480	Db	1501	TGGATGGGACCCGAGGGAGAAAGGGAGATGGCTGACGGACAGGACGGATGGGG 1560
QY	715	GCTGGGGACCGGGTATGGCTTACCTGATGAGCTTGGCAAATTAGCAACA 774	Qy	1777	GATCTCCGTGAGGACGCACTGGCAGTGGCAGTGGCTTACTGATAACCCTTCCGGCATGGCACACCCAG 1836
Db	481	GCGGTGGGGCATGCCATCACTTCCGAGGGCGAGCTGGCTGGGG 540	Db	1561	TGGATGGGACCCGAGGGAGATGGCTGACGGACAGGACGGATGGGG 1620
QY	775	GAAGCATCTCGTGAAGCTGAAGGGTTTGTGCTTACCTGATGAGCTTGGCGGTATATGTCGAACGTGCT 834	Qy	1837	TCTTGTCTGGCAGCCGAGTGGCTCGCTCATTCGCACTGAAAGCCGCTGGCG 1896
Db	541	GAGGGCGAGCGGAGGGCCACGGCCCTGGCAACGGGAGGTATCTCGAGAAAGATG 600	Db	1621	AGCGTGTGCCCCGGATCGCTGATGCAAGGTCAAGGTCTATGCG 1680
QY	835	GTGATTAAACCCCTAGGATATTGAAAGTGCAGATCCTTGGGATCACACTGGAGAAGTTGTA 894	Qy	1897	AAGCTGACTCCTGAGGATCCGCTGGGACAGGGCTGCGGAGGGATGGCG 1956
Db	601	ATCCAGGGCGGGCCACGTGAGGTGCAATCTCGGAGAATACGGCGATCTAC 660	Db	1681	GCAGACCTGGGCTCTCTCGGGRGAATGCTGGGGCTGGGCAATCGGGCTGCC 1740
QY	895	CACTTTATGAAACGTGACTGCTCACTGAGGTCGTCAACCAAAAGTTGTCGAATTGGCG 954	Qy	1957	ATGCGTTCTGAGGATCCGCTGGGAGGTGGCTGAGGGCTACCGATCTCCG 2016
Db	661	CATCTCTACGAGGGCAACTGGCACCGTGCAGGGCAACCGAGGGCTGGAGGG 720	Db	1741	TATCGCTTCCCTGAGGAATGTCCTGGGGCTGGGCAATCGGGCTGCC 1800
QY	955	CGAGCACAGCATTGGATCCAGAACTGGCATTCGCAATTGGGGATGGCAACGGTTC 1014	Qy	2017	AATGTAACATTAGATGCTGCTGGGATACACCGTGGGATACACCCGGTACCCA 2076
Db	721	CCGGCCCTTATCTCACCGAGGGCAAGGGCAACGGGCTGGGATCGGAGCTCGGGGG 780	Db	1801	AACGTCATGACGGAGATGCTGGGGCTCTCGGAACACTAACCCC 1860
QY	1015	TGCCGCTCCATTGGTACCCGGGGAAACCGTGGATTCTGGTGCAT---GAAAG 1071	Qy	2077	GACTCGTCTGGGGCTGGGAGGTGGCTGGGAGATCTCCGG 2136
Db	781	TGGGCCATGTGAATTACGAAATCGAGGTCGAGGGCAATCGGGGCAACCGAGGG 840	Db	1861	GACAATGTCGGGGCTGGGCAACCGGGAAACCGGGCTGGGCAATCGGG 1920
QY	1072	GGCAACCACGGTCTTCATCGAAATGAACCCACGGTATCCAGGGTGAACGGTGAACCGAG 1131	Qy	2137	ATCTTCGAGCGGCTAACGACGTTCCAGATGGCTGGGATCTCTGATCCGAG 2196
Db	841	GAGAAATTCTATTTCATCGAGGTCGAAATCGGGGCAATCGGGGCAACCGAG 900	Db	1921	GTGTCGACTCGCTCAACTGGGACAGATGGCTGAGAACATGGATGGTGTGAG 1980
QY	1132	GAAGTCACCGAGGTGACCTGGTGAAGGGCAAGATGCTGGCTGGCTGG 1191	Qy	2197	ACCAACACGGGCTAGCCGGATTACTACCTAAAGATGGCTGGGATCTCTGATCCAAAT 2256
Db	901	GAAGTGAACGGGCATCGACATCGTGCATCCGAAATCCGAGATCGGGCATCGGG 960	Db	1981	GCAACA---AGGCTGCGGAGGACATGGCTGATCGCTGATCCGGAC 2037
QY	1246	TGCCGCTACACCGGAAAGATCCAAACAGGTTCCGGCAGATAACGGAAACTATCACC 1305	Qy	2257	GAAAGCTCTAACATTAGATGCTGAACTACTATGTCGGGCTGGGATGGCTGG 2316
Db	1021	TGCCGCTACACCGGAAACGGGATGCCGAGGACATCGTGCATCCGAACTACGGCG 1080	Db	2038	CGCTCCAAATAAGATGCTGAACTACTATGTCGGGCTGGGATGGCTGG 2097
QY	1306	GGTACCGCTCACAGGGAGGATCCGAGGAGGATCCGAGAACAAATTCTCGACTGGT 1362	Qy	2317	GCTAACATCTGGCCATTAAAGGATGGCTGGCTGCTGCTGATCCGGAC 2376
Db	2158	CTGGTGAAGGGCTGGAGGGAGGAGGATGGCTGGGCTGGGATCCACCCAGGACAG 2217	Db	2098	GGGATGTCGGGCTGGGCTGGGATGGGACATGGGGCCGGCTGGGATCCGG 2157

Qy	2437	GGGGTGGCCAGCTGCAACCTTAACCTTGTGAGTCAGCTCAAGCTGGCAGATGCTGGTGCAC 2496	Qy	3469	GATGAGGTCAAGGGCTGGAGATGCCAGTCAGTCAGGCTATGAAAGATGGAAAGCAACA 3 528
Db	2218	AGGGAATTGCGGGGGCACCGTGTGCGATGCCGGCTGCGATGCCGGT 2277	Db	3295	CAGAAGGTGAAGGCCGATCTCCTCGTACCATCGGATGCCGGGG 3 354
Qy	2497	GGTGTTCGCAACCCTGTCGGCACCACTCCAGCCATCCCTGTCTGCCATTGTTGCT 2556	Qy	3529	ATCACTGCTTGTGTTGACGCCAAATCGATCGGTTGGTCTGCAACGAAGGTG 3 588
Db	2278	GGGGGATGGACGCCCTCTGGGGACCTCGCAGGCTCGCTGCCATCGTCGAG 2337	Db	3355	CTCATGCCAACCGTGGCCACCGTGAAGGCTGTCATGTCGGGCGGAGATC 3 414
Qy	2557	GCATTGCGCAACCCGTGCGATAACGGTTGAGCCTCGAGGTGTTGACCTCGAG 2616	Qy	3589	GAAGGTGGGACTTGAT 3605
Db	2338	GGGCTGAAGGCCACCCGACACGGGCAACGGGCTCGACATCGGGGAGATCTCG 2397	Db	3415	GGGGGAAGGACTGCT 3431
Qy	2617	CCGTACTGGAAAGCACTGGGGGACTGTACCTGCCATTGAGTCGGTGGAAACCCAGGCCA 2676	RESULT 13		
Db	2398	GACTACTGGGCCATGTGCGCCACCGATTCGGCTTGCCCTCGGCC 2457	US-10-369-493-35714;		
Qy	2677	ACCGGTGGCTTACCGCACGAAATCCAGGAAACTACGTTGTCACCTGCGCACAG 2736	; Sequence 35714, Application US/10369493		
Db	2458	GCCTCGAGGCTCATCTGCACGAGATGCCGGGGCAAGTCACCAACTCAAGGGCAG 2517	; Publication No. US20030233675A1		
Qy	2737	GCCACCGGACTTGGCCTTGGGATCGTTGAACTCATCGAAGACAACTACGAGGCCGTT 2796	; GENERAL INFORMATION:		
Db	2518	GCGCGCTCATGGGCTCGAGGAACGGTGGTCGAGCTGGCCATGCCGACGCG 2577	; APPLICANT: Cao, Yongwei		
Qy	2797	AATGAGATGGTGGGAACCAAGGTCAACCCATCTCCAAAGTTGTTGGACCTC 2856	; APPLICANT: Hinkle, Gregory J.		
Db	2578	AACCGGATGTTGGGACATCGTGAAGGTCAAGCCCTGTCGAAAGTGGCTGGGACATG 2637	; APPLICANT: Slater, Steven C.		
Qy	2857	GCACTCCACCTCGTGGTGGGATCCAGCAAGACTTGGTGGCATCCACAAAAAG 2916	; APPLICANT: Goldman, Barry S.		
Db	2638	GCGCTGATGATGGTGGGCAAGGGCTGACGGGAAAGAGGTGAGGATCCCAGGGTCGAG 2697	; APPLICANT: Chen, Xianfeng		
Qy	2917	TACGACATCCAGACTCTGTCACTCGGTTCTGGACATGGTCAACCTCCAGGT 2976	; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF		
Db	2698	GTGAGCTTCCGGACTCGGTCATCGGACATGTGCAAGGGCAATCTCGGCCAGCGGC 2757	; FILE REFERENCE: 38-1052052) B		
Qy	2977	GGCTGGCCAGGCCACCTGGCACCCGGCACCTCTGACGGAACTCTCGAACCGCTC-----	; CURRENT APPLICATION NUMBER: US/10/369, 493		
Db	2758	GGCTGGCCGGATCTGGGAGCTCGGCGACCTCTGACGGAACTCTCGAACCGCA 2817	; CURRENT FILING DATE: 2003-02-28		
Qy	3021	-----CGAAGGCAAGGGCACCTCTGACGAAAGGTGCTGAAGGGCAGGGCACCCCTCGAACCG 3054	; PRIOR APPLICATION NUMBER: US 60/360, 039		
Db	2818	CGGGGGCGCATCTGGCGCCGGGAGCATCGGAGCCGGGCGAGGGCTCGGGAG 2877	; NUMBER OF SEQ ID NOS: 47374		
Qy	3055	GAAGAGCAGGGCACCTCGAGCTGATGATCCAAGGAACGTCGAAATAGCCCTAACCG- 3113	; PRIORITY FILING DATE: 2002-02-21		
Db	2878	ATCAAGCAGGGGAGACGGATCCGGCTCGACACAGGGCTCGATGCCAGGGATCTGAACGGC 2937	; SEQ ID NO: 35714		
Qy	3114	-CCTGCTGTCGGTGGATGATCGTGAATCTCTGAGGCTGGCTGGCAAC 3171	; LENGTH: 3459		
Db	2938	TACCTCATGTATCCAAAGGTCTCACCGGACTACCGGCCACAGGATCTACGGGCG 2997	; ORGANISM: Mesorhizobium loti		
Qy	3172	ACCTCTGGCTGGCAGATGTGGTGAATCTCTGAGGCTGGCTGGCTGGCAAC 3231	US-10-369-493-35714;		
Db	2998	GTGCGGAGCTGGCAGACCCGGACCTCTCTACGGGATGGGAGGATCTCG 3057	Query Match		
Qy	3232	ATCCGCCTGCCAGATGTGGCACCCTCAACTGCTTGTGGATGCCATCTCTGAGCC 3291	Best Local Similarity		
Db	3058	GCCGAAT--CGACCCCCGAAAGACGCTGAGATCGGGATGGGGAGAGCG 3114	Matches 1788; Conservative		
Qy	3292	GACGATAAGGGTATGCCCAATGTTGGCCAACGTCACGCCAACATGCCGT 3351	0; Mismatches 1599; Indels 75; Gaps 11;		
Db	3115	TCGGACGAGGGGATGCCAAAGGGCAAGGGCCAGGGCTGAGTGGTCAATCGGGCAAT 3234	Db		
Qy	3352	GTGCGTGAACGGTCCGGTGAAGTCATGCCAACCGCAACGGAGATTCCTCCAAC 3411	229 GCATTCAAAAGATCTTGGTAGCAAACCGGGGAAATCGGGGCTTCGGTGC 288		
Db	3175	TCGGACGAGGGGATGCCAAAGGGCAAGGGCCAGGGCTGAGTGGTCAATCGGGCAAT 3234	4 GCCTACGAGATCCTCGTGGCCAAACGGTCAAAATCGGCATCTGGCTCTTCGGGG 63		
Qy	3412	AAGGGCCATGTTGCTGCCACCATCGTGAAGGTGTTGTCACC---GTGACTGTTGCTGAAGGT 3468	Qy	289 GCACTCGAAACGGGTGGAGCCACGGTAGCTATTACCCCCCGTGAAGATCGGGGATCATTTC 348	
Db	3235	CGGGCCCAATGTCGGGGCTGCCCTGGGGTCAAGAACACTGGGGAGATGCCAAGGG 3294	64 GCCTATGAACTGGGCTCAAAACCGTGGGATCTGGGCAATTCACCAAGGT 123		
Qy	3469	GATGAGGTCAAGGGCTGGAGTCAGTCAGGCTATGAAAGATGGAAAGCAACA 3 528	Qy	349 CACCGCTCTTGTGCTTGTGAAGCTTGTGAACTGGTACCTGGTACCC- -----GAA 390	
Db	3295	CAGAAGGTGAAGGCCGATCTCCTCGGCAATCGGCTGGGG 3 354	Db	124 CACCGCTTCAGGGCGACGAGGCTACAGGTGGGCACTGGGCGCTC 183	
Qy	3529	ATCACTGCTTGTGTTGACCTGCCAAATCGATGGCTGGCTGGCTGG 3057	Qy	391 GGCTCACCGCTCAAGGGTACCTGGGACATCGTGAATTTACGGTGCAGCTAAAAGGT 450	
Db	3355	CTCATGCCAACCGGCAATCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 3057	Db	184 ATGGGGCGATGCCATCCACCCGGCTACGGGCTTCTGTCCGAAAGCCC 303	
Qy	3589	GAAGGTGGGACTTGAT 3605	Qy	451 AAAAGCAGATGCCATTTCAGGGCTTCTGCTGAAATGGCCAGCTGGCTGGCGC 510	
Db	3415	GGGGGAAGGACTCTGCT 3431	Db	244 GGCGGGATGCCATCCACCCGGCTACGGGCTTCTGTCCGAAAGCCC 303	
Qy	3589	GAAGGTGGGACTTGAT 3605	Qy	511 GAGGTGGCCAAAAGGGCATTACTTTAGGGCCAACCCAGAGGCTGGCTGGCCAGTTGGGGAA 630	
Db	3415	GGGGGAAGGACTCTGCT 3431	Db	304 GCCTCGGCGCAAGGGGATCACCTCATGGCCATTCGGCTGCTGCTGGCTGGCTGGCGC 363	
Qy	3589	GAAGGTGGGACTTGAT 3605	Qy	571 GGTGATAAGCTCTGGCTGGTAACCCGCGGAAAGAAAGGTCTGGCTGCTGGCTGGGGAA 630	
Db	3415	GGGGGAAGGACTCTGCT 3431	Db	364 GGCAACAAGGGTGGCGGGCAATCTGGCCATTCGGCTGCTGCTGGCTGGCTGGCGC 423	
Qy	3589	GAAGGTGGGACTTGAT 3605	Qy	631 TCCACCCC---GAGCAAACATCGTGAAGATCGTAAAGGGCTGAAGGCTAC 687	
Db	3415	GGGGGAAGGACTCTGCT 3431	Db	424 ACCATCGGTTGCCCTGGGGTCAAGAACACTGGGGAGATGCCAAGGG 493	

688	CCCATCTTGTGAAGGCAGTTGCCAAATTAGCAACAGAACATCTCGTGAAGCTGAAGGGCTTCGGC	747
484	CCAGTGATGCTCAAGGCCCTGGGGGGCATGGGCCATCGGCTCC	543
748	CCTGATGAGCTTCGCAAATTAGCAACAGAACATCTCGTGAAGCTGAAGGGCTTCGGC	807
544	GAGGCCGATCTGGCCCGTCAAGGCAAGGGCAAGGGGAGGGAAAGGCCATCGGCTCC	603
808	GATGGCGGGTATATGTCGAACGTGCTGTGATTAAACCCTCAGGATATTGAAGTGCAGATC	867
604	AAGGACGAGGTCTATCTGAAAGCTGATCGAGGCCACGTCAGGTGAGGG	663
868	CTTGGCGATCACACTGGAGAACGTTGTAACACCTTATGAAACGTGACTGCTCACTGCAGCGT	927
664	CTTGGCGACACGGCATGGCAATGCCGTGACCTGAGGCCACTGTCGATCAGGCC	723
928	CGTCACCAAAAGTTGTCGAATTGGCCAGGCAAGGATTGGATCCAGAACTGCGTGAT	987
724	CGCAACCAGAAGGTCGTGAGGGGGCGCCCTATCTGAAATGTCGAGGGGAG	783
988	CGCATTTGTGGATGCCAGTAAGTTCTGCCATTGGTTACCGGCCGGGAACC	1047
784	GAGCTTTGGGCTACGGCTGAAGATCGCGGAGACAGCTATATGGCGCCGGACG	843
1048	GTGGAATTCTGGTCAATTGGCAACCAACCGTCTTCATCGAAATGAAACCCACGT	1104
844	GTGAGTTCTGGGATGCCGATAACGGAAATTCTATTCATCGAGGTCAACCCGGCG	903
1105	ATCCAGGTTGAGCACACCGTGAAGTAAGTCACCGAGGTGGCACCTGGTGAAGGGCAG	1164
904	ATCCAGGTTGAGCATACCGTCACCGGAGCAGGTGACCCGATCGATATCGTCAAGGGCAG	963
1165	ATGCGCTTGGCTGGTGCACCTTGAAAGGAATTG-----GGTCTGACCCAAGAT	1215
964	ATCCACATCCTCGACGGCTTCGCCATCGGCAACACGGCATCCACCGGAAGATCCAAAC	1023
1216	AAGATCAAGACCCACGGTGCACACTGCAGTGGCGCATCCACCGGAAGATCCAAAC	1275
1024	GATATCAGGCTGAACGCCATGCCCTGCAAGTGGCATCACCGAGGATCCGAGGCAC	1083
1276	GGCTTCCGCCAGATAACCGGAACTATCACCGCTACCGGCTCACCGGGAGCTGGCGTT	1335
1084	AATTTCATCCCCGACTATGGCCGATCACCGCCTATCGGGCTTCGGGCATC	1143
1336	CGTCT---TGACGGTGCAGCTCAGCTGGGAAATCACCGCACACTTGACTCCATG	1392
1144	CGGCTGGATGGGGCACCGCCTATTCTGGGGCATCACCGCCTTCAGATCGCTG	1203
1393	CTGGTCAAATGACCTGCCGTGGTCCGACTTTGAAACTGCTGTTGCTCGTGCACAGGGC	1452
1204	CTGGAGAAGGTGACGGCGTGGGGCGGAGACGGCCATGCCGACCCATGAAACCGG	1263
1453	GGGTTGGCTGAGTTCACCGTGTCTGGTGTGCAACCAACATTGGTTCTGGTGGTGC	1512
1264	GGCTGGCGAATTCCGCATTGCCGACCAACCTCACCGACCAAGTCACTGACACGCC	1323
1513	CTGGAGAAGGGACTTCACTTCCAAGGGCATGCCACCGGATTCACTGCCGATCCCC	1572
1324	ATCAACCACCCGAGCTTCGCCGACAATTCTACACGACCAAGTCACTGACACGCC	1383
1573	CACCTCCTTCAGGCTCACCTGCTGATGAGCAGGACGGCATCCTGGATTACTTGGCA	1632
1384	GAGCTTCCAGGGTCAAGGGCCTTCAGGGGAGACCAAGCTGCTCAACTATCTGGCC	1443
1633	GATGTCACCGTGAACAAGCCTCATG-----GTTGCGATAAGGATGCTCC	1686
1444	GATGTCAGGGTCAACGGCCATCCCGAGCGGGAGACGGGAGGGCGATGGC	1503
1687	ATCGATAAGCTGCCTAACATCAAGGATCTGCCACTGCCACGGCTG	1746
1504	GCCGCAACGGGTCTGCCCTATCTCAACGCAATGTGCGGAAAGGCTG	1563
1747	AAGCAGCTTGGCCAGCCGGACTGGCAGGACTGGCAGTTCTCCGTGATCTCGTCA	1806

Db	2641	ACGCCGCTCATCCAAGGTCTGGCGACATGGCCCTGATGATGGTCAGCCAGGACCTGACC	2700
Qy	2887	CCAGCAGACTTGTGCCGATCCACAAAGTACGACATCCCAAGACTCTGTCAATGGCGTTTC	2946
Db	2701	GTCGCCGATGTGAGAACCCGGCAGGGATTGGCTCCGGACTCGTCTCGATG	2760
Qy	2947	CTGGCGGGCGAGGCTTGTAACCCTCCAGGTGGCTGGCCAGGCCACTGGCACCCGGGCA	3006
Db	2761	CTGCGGGCGATCTCGGCCAGTGGCCGGGTTGGCGGGCTGAGAAGAGGGCG	2820
Qy	3007	CTGGAAGGCCGCTCCGAAGGCCAGGCACCTCTGACGGAAAGTTCCCTGAGGAAGGAGGGCG	3066
Db	2821	CTGAAAGGCCAGGCGATCACGGCACGGCCAGGCTGGCTCAAGGCCGGGATCTC	2880
Qy	3067	CACCTGACGGCTGATGATTCCAAGGAACCGTCGAAATAG-----C	3105
Db	2881	AAGGCCAGCCCAAGGAGATCGAGGAAAGCTGGAGGCCAAGGCTCTCGGAATAAGGAATTTC	2940
Qy	3106	CTCAACCGCCCTGCTGTCGGCAAGGCCAACCGGAAGAGTTCCCTGAGCACCGTCGCCGCTTC	3165
Db	2941	GCCTCCTGGCTGATGTTACTGACTTGCCGGCAAGGAACCTAC	3000
Qy	3166	GGCAAACACCTCTGGCTGGATCGTGAATTCTTCTACGGCCTGGATGGATCTCT	3225
Db	3001	GGCCCGGTCAGGTCCTGCCGACGCCACCTATTCTACGGCATGAAATGGAAAGACGAG	3060
Qy	3226	ACTTTGATCCGCCCTGCCAGATGCGCACCCCACCTGCTTGTGGATCTCT	3285
Db	3061	ATCTTCATCGACAT--CGAGAAGGGTAAGACGCCGCTGGTCTGGCTGCATCGGC	3117
Qy	3286	GAGCCAGACGATAAGGGTATGGCAATGTTGGCCAAACGTCACGGCCAGATCCGCCCA	3345
Db	3118	GATGTGGACGACAAGGGCATGGTCACGGTGTCTCGAGCTCACGGCCAGGGC	3177
Qy	3346	ATGGGTGTCGGTGACGGCTCCGGTGAAGTCTGTCACGGCAACCGAGAA---AAGGCAGAT	3402
Db	3178	GTGAAGGGTGGCCGGCATGGGGGCAAGGGCCCTGGCTGTCACCGGTAAAGGCCGAG	3237
Qy	3403	TCTCTCCAACAAAGGCCATGTTGCTGCCACCATCGCTGGTGTGACT---GTT	3459
Db	3238	CCTGGCAACGGGCAATGTGGGGCATGGTGGGTGACGTGCTGGCTGTTTCGGTC	3297
Qy	3460	GCTGAAGGTGATGAGGTCAAGGGCTGGAGATGCACTGTCGCAATCATCGAGGCTATGAAAGATG	3519
Db	3298	GCCACGGGCAAGGGTGAAGGGTCAAGGGCTGGTGAACGGCAAATCGATGTCGAGGCGATGAAAGATG	3357
Qy	3520	GAAGCAAACAAATCACTGCTTCTGTTGAGGCCAAATCGATGTCGAGGCTGGCTGCTGGTCAAGGCCGGC	3579
Db	3358	GAAACGGGGCTGGCATGCCGAGGGTGAACGGCACCGTGGCTGGTCAAGGCCGGC	3417
Qy	3580	ACGAAGGGTGGAAAGGTGGGACTTGTGATCGTCGTTCTAA	3621
Db	3418	GACCAAGATCGATGCCAAGGGATCTGCTGATAGCCCTTGCTGA	3459

QY	1174	GCTGCTGGTGCACCTT-----GAAGGAATGGGTCTGACC---CAAGATAAGATCAAG	1224	QY	2236	GGTGTATCTCTGATCCAATGAAAAGCTTACACCCCTGGATTACTACCTAAAGATGGCA	2295
Db	967	CTCGAAGGAGGGCCATCGGCACGGGGAAATCCGGCAGGGAAAGATTCATCCGC	1026	Db	2044	GGCGATCTCTGAAATTGGCACGTCACATCTGGCCGTCACATCTGGCTGGCTGGCTT	2103
QY	1225	ACCCACGGTGCAGCATGGCAGTGGCCGATCAACCACGGAAAGATCCAACAACGGCTTCGGC	1284	QY	2296	GAGGAGATCGTCAAGTCTGGGCTCACATCTGGCATTAAAGGATATGGCTGGCTGGCTT	2355
Db	1027	CTCAACGGCCATGGCTGCAGTGGCGCATCAAGACCGGAAGACACAAATTTCATT	1086	Db	2104	GTGAGCTGGAAAGGGCCCATATCATGGCGTCAAGGATATGGCTGGCTGGCTG	2163
QY	1285	CGAGATACCGGAAACTATCACCGCGTACCGGCTAACCGCACACTTTGACTCCATGCTGGTGA	1344	QY	2356	CGCCAGCTGGTAACCAAGTGGTACCGGACTGGCCGTTGAATTGAGTCTGCCAGTG	2415
Db	1087	CGGACTATGGCGTATTACCGCCTATCGCTGGCTTGCAATCCGGCTGGAT	1146	Db	2164	AAACGGCGCCAGGGTCTGTCAGGGTGTGGCTGGAGGGACCGTGGCAGCTCAA	2223
QY	1345	GGTG----CAGCTCAGCTCGGTACCGGAAATCAACCGCACACTTTGACTCCATGCTGGTGA	1401	QY	2416	ACGTGCAACCCACGGACACTGGGGTGGCCAGCTGGCAACCTAACCTTGCTGGCT	2475
Db	1147	GGGGCACTGGCTTACCGGCTCATACCGGTTGGCTGGCAAG	1206	Db	2224	CACTCCACACCCATGATACTGTCGGGATTCGGGCAATACGTGCGAGGCC	2283
QY	1402	ATGACCTGGCGTGGTTCGACTAAACTGCTGTTGCTGGTGGCTGGC	1461	QY	2476	CCTGGTGCAGATGCTGGTGAACGGTGGCTTCCGCACACCAACTGCTGGCACCAC	2535
Db	1207	GTCACGGCTGGGCTGGGCGGGATGAGGGATCAAGGGCATGGCTGGC	1266	QY	2536	TCCCTGTCGCCATTGGTGCATTGGCACACCCGTCGGGATACGGTCTGGCACCAC	2595
QY	1462	GAAGTCACCGGTGTCTGGTCAACCAACATTGGTTCTGGTGGTGGGAA	1521	Db	2344	TGCCCTGGCTGACGCCGTCATGGATGGCTGGGATTCGGGAAACGGGATCGAT	2403
Db	1267	GAATTTCGTATCCGGGGCTGGGACCAACCTCATCGCTTCATCGGTCA	1326	QY	2596	GAGCTGTGTTCTGACCTCGGCCGATTTCTCTTCTGACCTGGGACTGTGAC	2655
QY	1522	GAGGACTTCACTTCCAAGGGCATGGCACCGGATTCAATGCCGATACCCGACCTCCCT	1581	Db	2404	GAATGGATTGCCGATTTCCTCTATGGGAAAGCGCTGGCAATCAATATGCCGTTTC	2463
Db	1327	GACAGTTCCGAAACACACCTATACGACGGCTTCATCGATTGAGGGTGTTC	1386	QY	2656	GAGTCCTGGAAACCCCCAGGGCAACCGGCTGGCTTACCGCCACGGGAGACAG	2715
QY	1582	CAGGCTCACCTGCTGATGAGCAGGGACATCCTGGATTACTGGCAGATGTCACC	1641	Db	2464	GAGAGTGCACCTCAAGGGCTGGCTGGAAAGTCTATCTGCATGAAATGCCGCTGG	2523
Db	1387	GCGCAGGTCAAGGTCAAGGACCCGACCAAGGGCCATGGCTGGGATGTGACC	1446	QY	2716	TGTGCAACCTGCGTGCACAGGCCACCGGACTGGCCTTGGGATGTTGCAACTCATC	2775
QY	1642	GTGAAACAGCCTCATGGT-----GTGCGTCAAGGATGGTGCAGCTCTATGATAAG	1695	Db	2524	TTCACCAACCTCAAGGAACAGGCACGTTGGCTGGCTGGCTGGCTGG	2583
Db	1447	GTCAATGGTCACCCAGAAACCAAGGGTCTGGGAAAGGGGGAAAGCCC	1506	QY	2776	GAAGACAACCTACGGAGCCGTTAATGAGGATGCTGGGACTGGCCAAACGATG	2835
QY	1696	CTGCCCTAACATCAAGGATCTGCCACTGCCAACGGGGTTCCGGTGAAGCAGCTT	1755	Db	2584	GCGCAGGCCTATGGCGGACCTCGGACTCCACCTGGGATGTTGGGATTCAGGAG	2643
Db	1507	ATCGTGCCTATATGATGGCCGACGGCCACCAAGGCAATTGGCTGGACAAAGCTT	1566	QY	2836	TCCAAGGTTGGTGGGACCTGGGACTGGGCTGATGATGGTGGGATTCAGGAG	2895
QY	1756	GGCCCAAGCCGCTTGGCTCGTGAATCTCCGTGAGCAGGCACTGGCAGTTACTGATA	1815	Db	2644	TCCAAGGTTAGTCGGGCAATGGGCTGATGATGGTGGGATGGCTGGCGAT	2703
Db	1567	GCCCCTAACGGCTTGGGACTGGGACTGGCAACGAAAAGGGCTGGCTGGGATAG	1626	QY	2896	TTTGTGCGGATCCACAAAAGTAGCAGACATCCGACACTCTGTCATCGGCTGG	2955
QY	1816	ACCTTCCGGGATGCAACCGACTGGCTGGCTGGGACCCGAGTCGGCTCATTGGACTGAAG	1875	Db	2704	GTCGAAAACCCCTGACCGTTGAAAGTGTGCTGGTATCGATGCTGGCTGAAGGGT	2823
Db	1627	ACCATGGGGACGGACACCGACTGGCTGGCAAGGCTGGCTGGCTGGGATAG	1686	QY	3016	CGCTCGGAAGGGCAAGGCACCTCTGACGGAAAGTCTGGCTGGCTGGGG	3058
QY	1876	CCTGGGGAGGGCGATGGCGTGGCAAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	1935	Db	2824	GAAAAGCCTTACACGGTTGTCGGTTGGGAGATGCGATCTCGATGCGAA	2883
Db	1687	CGCGTTGGCAGGGTTATTCCAAGGGCTTCCGGCAAGCTGGCTGGCTGGCTGG	1746	QY	3059	AGCAGGGGCACTCTGACGGCTGATGCTGGCTGGCTGGCTGGCTGGCTGG	3114
QY	1936	GCGCGGACCTACGATGGCGATGGCGTGGCTGGCAAGGCTCGAC 1995		Db	2884	CGGAAGGTGATCGAGACCAAGCTGGCAAGGTGCTGGCTGGCTGGCTGG	2943
Db	1747	GTCGCGACCTTCGACGCTCAATGCCGCTAACCTGGCCGAAAGCTGGCTGG	1806	QY	3115	CTGCTGTTCCCGAAGGCCAACCGGAAGGTTCTCGGCCAACACACC	3174
QY	1996	GAGCTGGGAGGGACATCTCCGCACTTCGCTGGCTGGCAAGGCTGGCTGG	2055	Db	2944	CTGATGTTACCGAAGGTGTTTCACCGCATGGCTATGGCTGGCTGGCTGG	3003
Db	1807	CTCATTGGCAAGGTGCGCCGAAACCTGGCTGGCATGCTTCGAGATGCTTCTG	1866	QY	3175	TCTGGGCTGGATGATGCTGAAATTCTCTGACGGCTGGCTGGCTGGCTGG	3234
QY	2056	GTGGGATAACCCCGTACCCAGACTTCGCTGGCTGGCTGGCTGGCTGGCTGG	2115	Db	3004	TCCGTGCTGCCACCCATGGCTATTCTGAGATGGCTGGCTGGCTGGCTGG	3060
Db	1867	GTGGGTTAACAGAAACTATCCCGATAATGCTGTAAGTATTTCGCTGGCTGG	1926	QY	3235	CGCCCTGCCAGATGTGGCACCCCACTGGCTGGCTGGCTGGCTGGCTGG	3294
QY	2116	TCCGGCCGGGACATCTCCGCACTTCGCTGGCTGGCTGGCTGGCTGGCTGG	2175	Db	3061	GGGATATCGAGGGAGGAAGACACCCGGGGTAGCCGAGGTGGCTATGGCTT	3120
Db	1927	GGGGGGCGTGCATCTTTCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	1986	QY	3295	GATAAGGGTATGCCAATGGCAACACGGCCAAACGTCAACGGCCAGAT	3354
QY	2176	GCAATCGAGCGCAGTCCTGGAGAACCTGGCTGGCTGGCTGGCTGGCTGG	2043	Db			
QY	1987	TCGATGGATGGCATTGGCTGGGAAACAAGCTCTGCTACACC		QY			

Db 3121 GATAAGGCATGGTACGGTGTCTCGAGATCAACGCCAGCCATCAAGGTG 3180
 Qy 3355 CGTGAACCGCTCC---GTTGAGTGTCAACGGCAGAAAAGGCCAATCTCCAAC 3411
 Db 3181 CCGGATCGGCCATGGGCTTCGGCTCTGGCTGACGCCAACCGGCAAT 3240
 Qy 3412 AAGGGCCATGTTGCACATTGGTGGTGTGTAC ---CGTACTGTTGCTGAAGGT 3468
 Db 3241 GCGTCCCATATCGGCCGATGCCCTGGTCAATCAACCGGGT 3300
 Qy 3469 GATGAGGTCAAGGGCTGGAGATGGCAATCATCGAGGTATGAAAGATGGAACA 3528
 Db 3301 CAGGAGTCAAGGCCGACGTGCTCTCGATCGAGCCATGAAAGATGCCAACGGG 3360
 Qy 3529 ATCACTGCTTCCTGTTGACGGCAAATCGATCGGTTGTTCTGCAACCGAAGGTG 3588
 Db 3361 CTGCATGCCAACGGCAAGGGCAAGGTCAAGTTCTGGTGAAGTTCTGGTCAACCAGATC 3420
 Qy 3589 GAAGGGCCGACTTGATGTC 3609
 Db 3421 GACGCCAAGGATTGTTGATC 3441

RESULT 15
 US-10-369-493-38504
 ; Sequence 38504, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; Hinkle, Gregory J.
 ; Slater, Steven C.
 ; Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (52052) B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 473-4
 ; SEQ ID NO 38504
 ; LENGTH: 3453
 ; TYPE: DNA
 ; ORGANISM: Agrobacterium tumefaciens
 US-10-369-493-38504

Query Match 17.0%; Score 617; DB 15; Length 3453;
 Best Local Similarity 51.6%; Pred. No. 1.2e-177;
 Matches 1776; Conservative 0; Mismatches 1590; Indels 75; Gaps 13;
 Matches 1776; Conservatve 0; Mismatches 1590; Indels 75; Gaps 13;
 Qy 238 AAGATCTTGGTAGCAAACCGGGAAATCGGGTCCGGTCAAGCTCGAA 297
 Db 13 AAAATACTGTTGCCAACCGATCGGAAATTGGGATCCGGTTCACGGAG 72
 Qy 298 ACCGGTGCAGGCCACGGTAGCTTACCCGGTGAAGATCGGGATCATTCCACCGCT 357
 Db 73 CTTGGGATCAAAACGGTGGGATTCGGGCAAGGACAAGCTGTTCCGGCTC 1.32
 Qy 358 TTGGCTCTGAAGCTGTCGGCATTTGGTACCC-----GAAGGCTCACCA 399
 Db 133 AAGGGGGATGAATCCATCAGGCGATCGGGCAAGGATATGGACCG 192
 Qy 400 GTCAAGGGTACCTGGACATCGATGAAATTATCGGTGAGCTAAAAAGTTAAAGGAGAT 459
 Db 193 ATCGAGAGTTATCTTTCGATCGAGGGTATCCGTGCTGAATAATGCCAGCTGGG 252
 Qy 460 GCCATTACCCGGATACGGCTTCCTGTCAAGCTTCCCCGGAGGTGTGGG 519
 Db 253 GCGATCCATCCGGTTATGGCTCTGGCAAGGCCCTGAGTTCTGGAGGGCTGCAAC 312
 Qy 520 GAAAACGGCATTACTTTATTGGCCCAACCCCCAGGGACGGATCCGGATTACTGGAGATGTCACC 579

Db 3113 AGGCCGGCATCACCTTGATGGCCAGACAGTGGCCAGCTGGCAACAG 372
 Qy 580 TCTCGCGGGTAACCGGCCAGAAAGGCTGGTCTGCAGTTGGGAATCCA--CC 636
 Db 373 GTCGGCGGCCAATCTGGGATTTGGTTGATGCCATCCGGCAACATCCT 432
 Qy 637 CGAGGAAAACATCGATGAGATCGTAAAGGCTGAAGGCCAGACTACCCCATTCTT 696
 Db 433 CTGGCTGAGATGCCGAGTGGGGCTATGCCGAGAAATGGTATCCGGCATG 492
 Qy 697 GTGAGGGCAGTGTGCCGGAAAGGCCAGTGGTTGCTCACCTGTGATGAG 756
 Db 493 CTCAAGGGCTCTGGGGCATCGGGGATGCCATTGCAAAAGGAAAGAT 552
 Qy 757 CTTCGCAAAATTAGCAACAGAAGGATCTGTGAAGGTGAAGGGCTTTCGGGATGGCGCG 816
 Db 553 CTCGCCCGTGAAGGTGACGGAAAGGCCGCTCTGGGGCATGTGAGGCGAG 612
 Qy 817 GTATATGTGCAAGCTGGTGTGTTGAGTGAAGTGGAGATCCCTGGCGAT 876
 Db 613 GTTATCTGGAAAAGCTGTCGAGGCAAGGCCATGTGAGGCGATCTGGCGAT 672
 Qy 877 CACACTGGAGAAAGTTGTACACCTTATGAAACGTTGCTCACTGCACTGCAACAA 936
 Db 673 ACGCATGGCAATTGTCGCACTGTGTTGAGGGATTGTTGATCCAGAGACGCCAATCAA 732
 Qy 937 AAAGTTGTCGAAATTGCGCCAGCACGGCATTTGATCCGAAACTGCGTGTATCGCATTTGT 996
 Db 733 AAGGTGTCGAGGCCAGCACCGTATCTGTCGAAGGCCAGGGCAGGGCAGGG 792
 Qy 997 GCGGATGCGATAAAGTTCTGCCGTCATTGGTTACCCAGGGCGGGAAACCGTGGAAATTTC 1056
 Db 793 GCCTATTCCCTGAAAGATGCAAGGCCAACACTACATCGAGGCCAGTGTCAAT 852
 Qy 1057 TTGTCGAT----GAAAAGGGCAACCACTGCTCTTCAATGAAATGAACCCACTGCTATCCAGGTT 1113
 Db 853 CTGATGGATGCCGATACGGCAATTCTACTTATCGAGGTCAATCCGGTATCCAGGTT 912
 Qy 1114 GAGCACACCGTGAAGAAGTCACCGGAGGTGGACCTGCTGGCTTG 1173
 Db 913 GAGCATAACCGTTACCGAAGTGTGACCCGATCGATGAACTCCAGGATCCATT 972
 Qy 1174 GCTGCTGGTCAACCTT-----GAAGGAATTGGGTCTGACCC---CAAGATAAGATCAAG 1224
 Db 973 CTGAAAGGAGGGCCATCGGCACCGGGAAATCCGGTGCCTCAAGGAGAAAGATCCGC 1032
 Qy 1225 ACCACCGGTGCAGGCACTGCACTGGCCCATCACACGGAAAGATCCAACACGGCTTCGGC 1284
 Db 1033 CTCAACGGCCATGCGCTGAGTGCCTGCATCACGACGGAAAGACCAATTCTATT 1092
 Qy 1285 CCAGATAACCGGAACTATCACCGGTCACCAGGGGAGCTGGCGTTGCTTCGGAC 1344
 Db 1093 CGGACTATGGCCGTTACCGCCATCGCTGGCTCCGGGATCCGGTGGAT 1152
 Qy 1345 GGTG----CAGCTCAGCTGGTGGAAATCACGGCACACTTGACTCCATGCTGGTGGAA 1401
 Db 1153 GGGGACAGTCGCTTACCGGGCCGAGGGGATGAGGCTCATCCCGTTATTACGATCCGGTGGCT 1212
 Qy 1402 ATGACCTGGCGGTGGTTCCGCAAGGGGAGCTGGCTGGTGGCTGGGGCT 1461
 Db 1213 GTCACGGCTGGGGGATGCCAACCTGCAACCTGCACTGGCTGGCTGGGGCT 1272
 Qy 1462 GAGGACTTCACCTCCAGGGGATTCATGGGATGCCAACCTGCACTGGCTGGGGCT 1521
 Db 1273 GAATTCTGATTCGGGGGATGCCAACCTGCAACCTGCACTGGCTGGCTGGGGCT 1332
 Qy 1522 GAGGACTTCACCTCCAGGGGATTCATGGGATGCCAACCTGCACTGGCTGGGGCT 1581
 Db 1333 GACAGTTCCGGAAACAAACCTTACGAGGGCTCATCGATTGAGGGGGATGTTGRTTC 1392
 Qy 1582 CAGGCTCCACCTGCTGATGAGGGACGGATCCGGATTACTGGAGATGTCACC 1641

Db	1393	GCGCAGGTCAAGGTCAGACGGCCACCAAGCTTCTGACCTATCTGGCGATGTGACC	1452		Qy	2716	TTCGCCAACCTCGTGCACAGGCCACGGCCACTGGCCTTGCGAATCGTTTCGAACTCATC	2775
Qy	1642	GTGAAACAAGCTCATGGT-----GTGCGTCAAAAGGATGTTGCAGCTCCTATCGATAAG	1695		Db	2530	TTCACCAACCTCAAGGAACAGGGCACGTGGCTGGTCTGGTCTCGAAAGCCGGTACGAGGTG	2589
Db	1453	GTCAATTGGTACCCAGAAACCAAGGGTGGGAAGGCGAACAGGGCGAACAGGGCGGCC	1512		Qy	2776	GAAGACAACTACGCCAGGCCATAATGAGATGCTGGGACGCCAACCAAGGTCAACCCATCC	2835
Qy	1696	CTGCCCTAACATCAAGGATCTGCCACTGCCAGGGTTCCCGTGAAGCAGCTT	1755		Db	2590	GCGCAGGCCTATGCCATGGCGATATCGTCAGGTCAAGGTGACGCCGCTCC	2649
Db	1513	ATCGTGCCTATATCGATGCCGACGCCCTGACGGCACCAAGGAATGTGGACAGCTT	1572		Qy	2836	TCCAAGGTTGTTGGCGACCTCGACTCACCTCGACTGGATCCAGGAGAC	2895
Qy	1756	GGCCCAGCCGCGTGTGATCTCCGTGACCGGCACTGGCAGTTACTGATACC	1815		Db	2650	TCCAAGGTTAGTCGGGACATGGCGATGGTGAAGCTGAGCCAGGACCTGAGCGAT	2709
Db	1573	GGCCCTAAGGCTTGGGACTGGATGCCAACGAAAGGGCGTGTGTCACGGATACG	1632		Qy	2896	TTTGGTGCCTGCATCCACAAAGTAGCAATCCAGACTCTGTCAATCGCGTCTGGGGC	2955
Qy	1816	ACCTTCCGGATGCCACCCAGTCTTGGTGAACCCGAGTCCGTCATTGCACTGAAG	1875		Db	2710	GTCGAAAACCTGACCGTGAAGTGTCCCTCCCGGACTCGGTGGTATCGATGCTGAAGGGC	2769
Db	1633	ACCATGGCGACGGACACCGTCCGTCGGCCACCCGGTCCGTACCCATGATATCGCC	1692		Qy	2956	GAGCTTGGTAACCCCTCCAGTGGCTGGCAAGGCCACTGGGACCCGGCACTGCAAAGGC	3015
Qy	1876	CCTGGGGAGGGCGTGCAAAGCTGACTCTGAGCTTCTGAGCTTGTGCGGG	1935		Db	2770	GATCTCGGTCAATCGCCGGTGGGGAGCTGGTGAAGGGTGAAGGGT	2829
Db	1693	CGGRTGCCCCAGGGTTTATTCCAAGGGCTTTCGAGCTTCTGTGCTGGAAATGCTGGGC	1752		Qy	3016	CGCTCCGAAGGAAGGCCACTCTGACGGAAAGTCTCTGAGGA-----AG	3058
Qy	1936	GGCGGACCTACGATGGGATGCCATTCTCTGGGATCCGGGGACAGGGCTCGAC	1995		Db	2830	GAAAAGCCTTACACGGTTCTGGTCCGGGTTCTGGTGAAGATGCCGATCTCGATGCGGAA	2889
Db	1753	GTCGACCTTCGACGTCCTCAATCGCTTCCCTGACCGAAGACCGTGGGGCTGTCA	1812		Qy	3059	AGCAGGGCACCTCGACGGTGTGATGATTCCAAGGAACGTCGCAATAGCCTAACCGC	3114
Qy	1996	GAGCTGGTAAACATTCACTGATGCCACCCGGCCGAAACACC	2055		Db	2890	CGGAAAGGTGATCGAGGACCAAGTGGTGAAGCTGGACTCTCGAGTTGCCTCTAT	2949
Db	1813	CTCATTGGCAAGGGTGGACATCTCCGGCAACCTGGCTGGTGGCCAAACGGC	1872		Qy	3115	CTGCTGTTCCGAACCCGAAAGAGTTCTCGAGCACCGTCTGCCAACACC	3174
Qy	2056	GTGGGATAACACCCGTACCCAGACTCCGTCTGCCCTGAGCTGGCCAGC	2115		Db	2950	CTGATGTTACCGGAAAGGGTGTCAACCGATTTCGCGCTGACCGCAGACATACGGCCGTC	3009
Db	1873	GTGGTTACAAAGAACTATCCGATAATGTGTGAGATGCTTCTGCGGGCAAGG	1932		Qy	3175	TCTGGCTGGATGATCTGTGAATTCTCTAGGGCTGGTGAAGGGCGGAGACTTTGATC	3234
Qy	2116	TCCGGGTGGACATCTCCGGCATCTCGACGGCCTTAACGGACGTTCTCCAGATGGTCCA	2175		Db	3010	TCCGTGCCCCACCCATGCTTATTCGCGATGGGATCTATGCTTAATCGGCT	3066
Db	1933	GGGGGGTICGATTTTCGCGTGAACCTGGGGAAATATGGGGTT	1992		Qy	3235	CGCCCTGCCAGATGGGCCAACCCCACTGCTTCTGGGATGCGATCTGAGCCAGAC	3294
Qy	2176	GCAATCGACGGCAGTCTGGAGACCAACACCGGGTAGCCGAGTTACTACCTAAAGATGGCA	2295		Db	3067	GCGGATATCGAGGGGAAAGACGCTTGTCAATCGTCAATCAGGGCTATGGGATGGGAAAGAG	3126
Db	1993	TCGATGGATGGGATTGGCAAGGAGAAAC---AGCTCTGGCGAACAAATATGCTCAAC	2049		Qy	3295	GATAAGGGTATGGCAATGGGCAATGGGCAACCGCAGAAAAGGCAAGGATTCCTCAAC	3354
Qy	2236	GTTGATCTCTGATCAAATGAAAGCTCACCTGGCATTAAGGATACTGGCTCTGCTT	2355		Db	3187	CCGATGCGCCCATGGGCTTGGCTGCGGCGCATCAAGGGCAATCCGGGAAT	3246
Db	2050	GGCGATCTCTGAAATTGGGACCTGGCAAGGAGAAACATCTGGTACACC	2109		Qy	3127	GATAAGGGCATGGTGAAGGGTGTCTCGAGATCAACGGCCAGGGCTGAGGT	3186
Qy	2296	GAGGAGATGGTCAAGTCTGGCTCACATCTGGCCATTAAGGATACTGGCTCTGCTT	2355		Db	3355	CGTGACCGCTCC---GTTGAGTGTGACCTGGGATGGTGTGTCAC---	3411
Db	2110	GTGAGCTGGAAAAGGGCGCCAAAGGTTCTGTTCAAGGGTGGGGCTGATGGCGATC	2169		Qy	3188	CGTGCCTCATGGGCTTGGCTGCGGCGCATCAACGGGCAATCCGGGTCTTCATCAACGGGT	3306
Qy	2356	CGCCCAAGTGGTAACCAAGCTGGTCACTGGGACTCTGGCCATTCGGCCAGTGG	2415		Db	3247	GCGTCCCATATGGGCGCTGGGCTGCGGCGCATCAACGGGCAATCCGGGTCTTCATCAACGGGT	3366
Db	2170	AACCGGGCGCCAAAGGTTCTGTTCAAGGGTGGGGAGCCGGTCTGGCGATC	2229		Qy	3469	GATGAGGTCAAGGCTGGAGATGCGACTGGCAATCTGAGGTATGAAAGTGGAAACA	3528
Qy	2416	CACGTGGCACACCCACGACACTGGGGTGGCCAGCTGGCAACCTACTTGTGCACTCAA	2475		Db	3307	CAGGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	3588
Db	2230	CACTTCCACACCCATGATACTGTGGCATTTCGGGCACTGGCCAGCTGGCTCTGGGT	2289		Qy	3529	ATCACTGCTTCTGTTGCGGCAAATATGATGCGGCTGCTGCTGCAACGAAAGGT	3367
Qy	2476	GCTGGTGGCAGATGGCTGTTGACGGGTGCTTCGGCAACCCTCCAGCCA	2535		Db	3367	CTGATGCCGAGGGCAAGATCGCTGAGGTCTGGTGAAGGTTCTGGTGAAGGCGATC	3426
Db	2290	GCGGCGTGGCAGGGCTGGGCTGCGGAGTGGCTGGCAATACGGTCAAGGGTCTGG	2349		Qy	3589	GAAGGGGGGACTCTGATCGTC	3609
Qy	2536	TCCCTGTTGCTGCAATTGGTGTGCAATTTCGGCAACACCCGTGCGATACGGTTGGCCTC	2595		Db	3427	GACGCCAAGGATTGGTGTGATC	3447
Db	2350	TGCTTGGCTGATGTTGGAGGGCTCTGGGATCGGAGCGGATACGGGTCTGG	2409					
Qy	2596	GAAGCTGGCCAAACGGCCACTGGCTGCGGACTGGGAAAGCAGCTGTCACCTGCCCATT	2655					
Db	2410	GAATGGGATTCGCCGCTAAAGGGCTGCTGGCTGGCAATCAATATGCCGGGTTC	2469					

Search completed: March 24, 2004, 06:08:42
Job time : 1227 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
 Run on: March 23, 2004, 18:35:49 ; Search time 8670 Seconds
 (without alignments)
 12471.852 Million cell updates/sec

Title: US-10-045-072-1

Perfect score: 3621

Sequence: 1 tggggcggggttagatccctg.....tgatcgtagtcgtttcccaa 3621

Scoring table: IDENTITY_NUC

Gapop 10_-, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthu:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_p1n:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_png:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

ALIGNMENTS

RESULT 1
 AY408287 LOCUS 3537 bp DNA, VIRTUAL TRANSCRIPT, partial sequence, genomic
 DEFINITION Mus musculus PC gene, survey sequence.
 ACCESSION AY408287
 VERSION AY408287.1 GI:39764258
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3537)
 AUTHORS Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

JOURNAL 14671302
 PUBMED 2 (bases 1 to 3537)
 REFERENCE Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.8	16.8	3537	AY408287	AY408287 Mus muscu
2	606.2	16.7	3537	AY408285	AY408285 Homo sapi
3	442.4	12.2	3537	AY408286	AY408286 Pan trogl
4	432.2	11.9	2877	AK077665	AK077665 Mus muscu

JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	<pre> 1. . 3537 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1. .>3537 /gene="PC" /locus_tag="HCM3173" </pre>

JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
1.	.3537
/organism="Mus musculus"	
/mol_type="genomic DNA"	
/db_xref="taxon:10090"	
<1..>3537	
/gene="PC"	
/locus_tag="HOM3173"	
ORIGIN	
Query	Match Score 609.8; DB 29; Length 3537;
Best Local Similarity 48.5%; Pred. NO. 2.2e-131;	Mismatches 0; Indels 24; Gaps 6;
Matches 1361; Conservative 1361; Matches 1361;	Score 609.8; DB 29; Length 3537;
Y 233 TCAAAAGATCTTGGTAGCAAACCGGGCGAAATCGGGTCCGTGCTTCCGTGCCAC 292	QY 1310 ACGGTCACCCAGGGAGCTGGGTCAGCTCAGCTCGGTGGCGAAA 1369
b 110 TCAAGAAAGTAATGGTGGCCAACAGAGGTGAGATTGGCATCCGAGTGGTTCTGGTGC 169	Db 1190 TCGGAGTGGCATGGCATGGCATGGCAC 1249
y 293 TCGAAACCCTGGCACCGGCAACGGTAGCTATTACCCCGTGAAGATCGGGATCATTCCACC 352	QY 1370 TCA---CCGCACACTTGACTCCATGCTGGTGAATAATGACCTGCGCTCCGACTTTG 1426
b 170 CAGAGCTGGGATACCGCACAGTGGCTACTCGGAGCTACCTGGTGGCTACTCGGAGGAC 229	Db 1250 TCATATCGCCCCACTATGACTCTGTCTGGTCAAGGTCAATTGCAACCGCAAGACC 1309
y 353 GCTCTTGTCTCTGAAGCTGTCCGCCATTGGTACCGGAAGGCTCACCAAGTCAAGGGTAC 412	QY 1427 AACTGCTGTGCTCTGGCACAGCGGCCGTTGGCTGAGTTACCGTGTGGTGC 1486
b 230 GGCAGAAAGCTGATGAAGCTTACCTATTGGCCGGTGGCTGACCTGTGAGGCTTACCT 289	Db 1310 CCACAGCTGCCACCAAGATGAGCAGGCCCTGGCAGTGGTCAAGGTAAAGN 1369
y 413 TGGACATCGATGAAATTATCGGTGCAAGCTAAAGTTAAGCAGATGCCATTACCCGG 472	QY 1487 CCAACATTGGTTCTTGGTGTGCTGGGGAAAGAGGGACTTCACTTCAAGGGCATCG 1546
b 290 TGCACATTCCAGACATCATCAAGGTGGCCAAGGAAATGGTGTAGATGGGGCATCTG 349	Db 1370 NNN 1429
b 533 CTTTTATTGGCCAACCCCAGGGTCTGGTAAAGGGGAAACGGCATTAA 532	QY 1547 CCACCGGATTCAATTGGCATTACCCGATCACCGCACCTCCACCTGGCTGATGAGGC 1606
y 350 GCTATGGTTCTCTAGAGGGAGACTTGGCCAGGGCAAGATGGTGTAGATGGGGCATCTG 349	Db 1430 NNN 1489
b 473 GATACTGGCTTCCTGTGAAAAATGCCAGCTGGCCAGGTGGGAAAGCAGGCTTA 409	QY 1607 AGGGACGGCATCTGGATTACTGGCAGATGTGCTGACCGCTCATGGTGTGGGTCTC 1666
b 593 CGGCCGGAAAGAAGGTCTGGTAAAGGGGAAATGGGAGACAAGGGTGGTCTGGGGTAA 469	Db 1490 NNN 1549
b 410 GGTTCAATTGGTCCAAGGCCAGGGTGGTCCAGGGTGTGATAAGTCTGGGATCTGGT 409	QY 1667 CAAGGAATTGGTGCAGCTCCTATCGATAAGCTGCCAACATCAAGGATC-----TGCCAC 1720
b 593 CGGCCGGAAAGAAGGTCTGGTAAAGGGGAAATGGGAGACAAGGGTGGTCTGGGGTAA 592	Db 1550 CTGTCAATTGTGAGCCCCAGGTCTGGGATCTGGTCTGGTGGCTGGCCATAGGCCAC 1609
b 470 CCATTGCCATCGCTGGGGCATGAGTTCTCCAGTGGTCCAGGGGACTTCCCCTAGCTCCC 529	QY 1721 TGCCACGGGTTCCCGTGAAGCAGTTACCTGATAACCACCTTCCGGATGCCAGCTT 1780
b 650 TCGATGAGATCGTTAAAGGGCTGAGTTGGCTGAAGGCCAGACTTACCCATCTGGCT 589	Db 1610 CTCCAGCTGGTTCAAGGACATCCTTCGGGATAGGGACACAAACCTTCCGGGATGGC 1669
b 530 TGCACGGAGGGCATGAGTTCTCCAAACACCTACGGCTTCCCTATTATCTCAAGGCCCT 529	QY 1781 TCCGGTGAAGCAGGCCACTGGCAGTTACTGATAACCACCTTCCGGATGCCAGCTT 1840
b 710 CCGGTGGGGGAGGGCTATGGTTGGCTGAAGGGCTTACCTGTGAGCTTCCGAAATTAG 769	Db 1670 TGCGGAATCACCGGGCTGGTGTGGATGGACACATGATCTCAAAAGATGGCC 1729
b 590 ACGGAGGTGGGGGAGGGCTATGGGGCTGGGATGGGGTATATGTCGAAC 829	QY 1841 TGCTTGGGACCCGAGTCCTCGCTCATTGGCAGCTGGGGCTGGGAGAC 1900
b 770 CAACAGAAGCATCTCGTGAAGCTGTAAGGGCTTTGGCGATGGGGTATATGTCGAAC 829	Db 1730 TAATGGCCACTAGGTGGCACACATGATCTCAAAAGATGGCCCTATGTTGCC 1789
b 650 ACACCCGGGCTTAACCTCGGAGCTTGGGGATGGGGATGGGATGGGAGA 709	QY 1901 TGACTCCTGAGCTTGTGGCTGGGGCTGGGAGCTAGGATGTGGGATGC 1960
b 830 GTGCTGTGATTAACCTCGGATATGAGCTGGGATCACACTGGAGAAG 889	Db 1790 ACTTCAACAAAGCTTCAAGGATGGGAGAACACTGGGAGA 1849
b 710 AGTTCAATTGAGAAGCCAAAGGACATTTGGATCOAGAATGGGGACAGTGGGAACA 769	QY 1961 GTTTCCTCTTGGAGATCGTGGGGACAGGGCTCGAGGCTGGGGATGCCGAATCT 2020
b 890 TTGTACACCTTATGAACTGGTCACTGGCTGAGCTGCTCACTGGCTGGGGCTGGGAG 949	Db 1850 GCTTCCTGTACAGGTGCCCCCTGGGGCTCAAGGCTCCAGGAGCTGGCATGCC 1909
b 770 TCCTGCACCTGTACGGGAGACTGCTCCATCCAGGTGATGGGGATGGGAGA 829	QY 2021 TAAACATTCAAGATGGTGTGGGGGATACCCGGCTACCTGGGAGCTGGCATGCC 2080
b 950 TTGCGCCAGCACGGATTGGATCOAGAATGGGGATGGGGATGGGAGA 1009	Db 1910 TCCCGTTCTCAGATGCTGGGGCTACACAACTACCCCTGACA 1969
b 830 TCGCCCTGCTAACCCACCTGGTACGGGAAACCGGGGACTCTGGCTCAAGGTGACTCTGTC 889	QY 2081 CGTCTGGCGGGGCAATTGGTCAAGGTTCTGTGAGGAAATGGTATGGGAGGTC 2140
b 1010 AGTTCTGGCTCCATTGGTACGGGAGACTGCTCCATCCAGGTGATGGGGATGGGAGA 1069	Db 1970 ACGTGGTGTCTTCAAGGTTCTGTGAGGAAATGGTATGGGAGGTC 2029
b 890 AACCTGCCAAGCACGGTAGGCTATGAGAACGGGGACTCTGGGACTAGGAGAACAGC 949	

REFERENCE AUTHORS	1 (bases 1 to 3537) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBLMED	14671302
REFERENCE AUTHORS	2 (bases 1 to 3537) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
JOURNAL PUBLMED	14671302
TITLE	Direct Submission (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES SOURCE	Location/Qualifiers 1..3537 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>3537 /gene="PC" /locus_tag="HCM3173"
ORIGIN	Query Match Best Local Similarity 16.7%; Score 606.2; DB 29; Length 3537; Matches 1365; Conservatve 0; Mismatches 1416; Indels 24; Gaps 7;
Qy	2381 TCACCGCACTGCCGATTAAAGATGGCAGAGGAGATCGTCAAGTCTGGGCTC 2320
Qy	2147 CTAATACTCACTGGAGTAACATGGCTTAGCTGAGAACTGGTGGCACTC 2206
Db	2321 ACATCTGGCCATTAAAGGATATGGCTGGCTTGCCAGCTGGTAACCCAAGCTG 2380
Qy	2207 ACATCCCTGTGCATTAAAGGACATGGGGCATCTCATACGGGGACTGGCTG 2146
Db	2261 AGCTTACACCCCTGGATTACTACCTAAGGATGGCAGAGGAGATCGTCAAGTCTGGGCTC 2320
Qy	2267 TCAGCTCCCTCCGGACCGATTCCCGATGCTGGCAGCTCCACTGCACATGATA 2326
Db	2438 CGGGTGGCAGCTGGCAACCTACTTTGTCAGCTGGCAGATGCTGTTGACGG 2497
Qy	2327 CAGGGGAGGGTGGCACGGCATGCTGGCAGCTGGCACAGGAGGGCTGATGTTGGACGG 2386
Qy	2498 GTGCTTCCGGACCACTGTTGGCACACCCTCCAGCCATCCCTGTCATTGTTGCTG 2557
Db	2387 TGGCAGTAGACTCCATGTCATGTTGGATGACCTCACAGCCAAAGCTCACAGCC 2446
Qy	2558 CATTCCGGCACACCCGCTGGGATAACCGGTTGGCTGAGCTCTGAGCTCGAGC 2617
Db	2447 GTACCAAAGGGACTCCTTGGACACAGGGTACCCCTGGAGCTGACTACAGTG 2506
Qy	2618 CGTACTGGGAAGCAGTGGGACTGTACCTTGCACTTGATTGAACTTGGCATTG 2671
Db	2507 AGTACTGGGAAGGGCTGGGACTGTACGGAGCTTGCACTGGCTACGGTACATGAAGT 2566
Qy	2672 GCCCAACCGGCTCGCTAACGGCCACGGGAGACAGTTGTCACCTGCGTG 2731
Db	2567 CTGGCAACTCCGACGGTGTATGAGAATGAGATTCAGGGGGCAGTACACCAACTGCACT 2626
Qy	2732 CACAGGCCACCGCAACTGGGCTTGGGATCGAAAGACAACACTACGGCAG 2791
Db	2627 TCCAGGCCCATAGCATGGGGACCTCATGGTGGCTCAAGGTCAAGGGCTATGTTGG 2686
Qy	2792 CGGTTAATGAGATGGCTGGGACGCCAACCAAGGTCAACCCATCTGCAAGGGTGTTCGGCG 2851
Db	2687 AGGCTAACCGATGCTGGGGACCTCATGGTGGCTCAAGGTGACACCCTCCAAAGGACTTGGGG 2746
Qy	2852 ACCTCGGCACTCCACCTGGGCAACTCTGGGATCCAGGACTCCAGGATCCAC 2911
Db	2747 ACCTGCCCAAGTTCATGGTGGCTCTGGGACCTCATCAAGGTGACACCCTCCAAAGGCTCAGGGCAG 2806
Qy	2912 AAAAGTACGACATCCCAAGGACTCTGTCATCGCGGACTTGGGATCCAGGACTTGGTAACCCCTC 2971
Db	2807 AAGAGCTGTCTTCCCCTGGCTCATGGTGGGAGTGGTGGCTCAAGGTAAAGGACC 2866
Qy	2972 CAGGTGGCTGGCCAGGCCACACTGGGCACTGGGAAGGCC 3016
Db	2867 ATGGGGGTTTCCCTGAGCCCTTCTGGCTCAAGGTGCTAAAGGACC 2911
Qy	3537 bp DNA linear GSS 15-DEC-2003
DEFINITION	Homo sapiens PC gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY408285
VERSION	AY408285
KEYWORDS	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Db	2867	ATGGGGTTCCCGAACCCCTTCGCTTAAGGTACTGAAGGACC	2911
RESULT	3		
AY408286	AY408286	3537 bp	DNA VIRTUAL TRANSCRIPT, linear GSS 15-DEC-2003
LOCUS	Pan troglodytes PC gene, genomic survey sequence.		
DEFINITION	Pan troglodytes PC gene, genomic survey sequence.		
ACCESSION	AY408286		
VERSION	AY408286.1	GI:39764257	
KEYWORDS	GSS. Pan troglodytes (chimpanzee)		
SOURCE	Pan troglodytes		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. (bases 1 to 3537)		
REFERENCE	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.		
AUTHORS	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBLMED	14671302		
2 (bases 1 to 3537)			
REFERENCE	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.		
AUTHORS	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
JOURNAL	Direct Submission		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
Source	1. .3537 /organism="Pan troglodytes"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9598" />3537		
	/gene="PC" /locus_tag="HCM3173"		
ORIGIN			
Query	Match Score 442.4; DB 29; Length 3537;		
Best Local Similarity 41.5%; Pred. No. 4e-92;			
Matches 1004; Conservative 0; Mismatches 1400; Indels 18; Gaps 6;			
Db	233 TCAAAAGATCTTGGTAGCCAACCGGGAAATCGGGTCCGGTGGCAGCAC 292		
Db	110 TCAAGANNGTCATGGGCCAACAGAGGTGAGATTGCCATCCGGTGTCCGGCTGCA 169		
Db	293 TCGAACCGGGCACGCCACGGTAGCTTACCCCGTGAAGATCGGGATCATTCACC 352		
Db	170 CGGAGCTGGCATCCGCACCGTAGCCATCTACTCTGAGGCCATCGGGCAGATGCC 229		
Db	353 GCTCTTTTGTCTGAAGGCTGTCGCAATTGGTACCGAAGGGCTCACAGTCAAAGGGTACC 412		
Db	230 GGCAGAAAGCAGATGAAGCCTATCTCATGGCCGGGCTGGAGGCCCTAAC 289		
Db	413 TGGACATCGATGAATTATCGGGCAGCTAAAGGATAAGCTTACCCGG 472		
Db	290 TGCACATCCAGACATCAAGGTGGCCAAAGGAACACAGTAGATGCCATTACCCCTG 349		
Db	350 GCTACGGGTTCCCTGTTGCTGAGGGACTCTGGCCAGGCTGCAAGNATGCCAGGT 409		
Qy	533 CTTTTATTGGCCAAACCCCAGGGTCTCTGATCTCACCCGGTGTGATAAGTCTCGGGGTAA 592		
Db	410 GGTTTATTGGGCCAACGCCAGGGTCCGAGAAGTGGGAGACAGGTGGAGCCCCGG 469		
Qy	593 CGCCGGAAGAAGGGCTGGTGGCCAGTTGGCCAGTCAAGGATCTGCCACT 649		

FEATURES	source	URL: http://fantom.gsc.riken.go.jp/ .
	Location/Qualifiers	
1.	.2877	
	/organism="Mus musculus"	
	/mol_type="mRNA"	
	/strain="C57BL/6J"	
	/db_xref="FANTOM DB:5730513C12"	
	/db_xref="MGI:2393843"	
	/db_xref="taxon:10090"	
	/clone="5730513C12"	
	/tissue_type="whole body"	
	/clone_Lib="RIKEN full-length enriched mouse cDNA library"	
	/dev_stage="8 days embryo"	
	<1: -2489	
	CDS	

/note="unnamed protein product; putative
pyruvate decarboxylase (MGD|MGI:97520, GB|NM_008797,
evidence: BLASTN, 99%, match=2877)"
/codon_start=3
/protein_id="BAC36939.1"
/db_xref="GI: 26346581"
/translation="VSEGQSILPDIGLQENIRINGCAIQCRVTTEDPARSFQPPDTGRI
EVFRSGEGMIGIRLDNAAFAQGAVISPHYDSSLVVKVIAHKGDKHPTAATMMSRALAAEFRV
RGVKTNIPEFLQNVLNQQFLAGTVDTQFIDENPELFQLRPAQNRAQQKILHHLGHVMVN
GPTTPIPVNVSPSPVPDAVPVVPPIGPPPAGFRDILLREGPEGFARAVENHQGLLLMDT
TFRDAHQSLILATVRTHDLKKIAPYVAHNENFKLFSMENWGGATFDVAMRFLYECPWRR
LQEELRELIPNIPEQMLLPGANAVGTYNPDNVVFKFCCEVAKENGMDVERVFDLSNYLP
NMLOGMEAAGSAGGVVEAAISYTGDVADPSRTKYSLEYMMGLAAELVRAGTHILCIKD
MAGLLKPAACTMLVSLLDRFPDLPLHIHTHDTSAGGVAAMLAQAQAGDVVDVAVDS
MSGMTSQPSMNGALVACTKGTPLDTEVPLERVFDYSEYWEGARGLYAAFDCTATMKGNSGN
SDVYENEIPGGQYTNLHFQAHSMGLGSKFKEVICKAYVEANQMLGDLIKVTPSSKIVGVD
LAQFMVONGLSRAEAQAEELSEPSSVVEPLGGYIGIPHGGGPEPFRSKVLDKLPLPRI
EGRPGASLPPNLKELEKDLIDRHGEETVTPEDVLSAMYPDVFQAQFKDFTATFGPLDS
LNTRFLQGPKIAEEFEVELLERGKTLHIKALLAVSDLNRAQORQVEFELNGOLRSILV
DTQAMKEMHFPKALKDVKGGQIGAMPKGVIDIKVAGDKVAGQPLCVCVLSAMKMETV

polyA_signal

Qy 1112 TTGAGGCACCCGTGACTGAGAAAGTCACTGGGACTCTGGTGAAGGGCAGATGGCCT 1171 Db 78 GCTGATGGACAGGACCTTCAGGGACGCCAACCAAGTCACTGTTGGCCACTCGTGTGGCAC 137
 Db 135 TCGAACATACAATTACCGAAGAATCACCGGTATCGATATCGTCGCTCAAATCCAA 76 Qy 1863 ATTGGCACTGAAGCGCTGCGGAGGGCGAGTGGCTAAAGTCGACTCCGTGATGGCTCGGT 1922
 Db 138 CCACGATCTCAAAGATGCCCCATATGTTGCCAACACTCAGGAAGCTCTTCAGGGAT 197
 Qy 1172 TGGCTGCTGGCAACCTTGAAAGGAATTGGGGTCTGACCCAAGATAAGATCAAGACCCAG 1231 Db 1923 GGAGGCTGGGGGGGACCTACGATGTGGGATGCGTTCCCTTGTGAGGATCCGTRG 1982
 Db 75 TCGCTGCAGGTGCCACTTGGAACTATTGGTTGATGCAAGATAAGATTACAACCTCGTG 16 Qy 198 GGAGAACTGGGAGGGCACGGTCCAGGTTGACGTGCCATGCGTCTCCTGTATGAGTGGCCCRG 257
 Qy 1232 GTGCAAGCACTGCACT 1246 Db 1983 GGACAGGGCTCGGAGGCTGCGGAGATGCCAGATGTAACATTCAAGATGCTGCTTCG 2042
 Db 15 GTTTCGCCATCCAGT 1 Qy 2043 CGGGGGCAACACCGTGGGATACACCCAGACTCCGATCTCCGACGGCCTTAACGAGCTC 2102
 Db 258 GGGGGGCTGGAGCTCCGGAGCTCCGGATTCACCCAGACAACATCCCAACATCCCT 317
 Qy 20881271 903 bp mRNA linear EST 16-AUG-2002
 LOCUS AGENCOURT 7978339 Lupski dorsal root_ganglion Homo sapiens cDNA
 DEFINITION clone IMAGE:6185002 5', mRNA sequence.
 BQ881271 GI:222273279
 BQ881271.1 EST.
 VERSION 1
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 903)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LILN at:
 http://image.llnl.gov/
 Plate: LLAM13575 row: b column: 11
 High quality sequence stop: 692.
 FEATURES source
 1. .903
 /organism="Homo sapiens"
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGGTCCG-3', and
 5'-GACTAGTTCTAGATCGGAGGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
 /lab_host="DH10B"
 /clone_1.lib="Lupski_dorsal_root_ganglion"
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCACGGTCCG-3', and
 5'-GACTAGTTCTAGATCGGAGGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
 ORIGIN Query Match 6.5%; Score 236; DB 13; Length 903;
 Best Local Similarity 57.4%; Pred. No. 5.2e-44;
 Matches 466; Conservative 0; Mismatches 340; Indels 6; Gaps 2;
 Qy 1743 CCTGAAAGCAGCTGGCCAGGCCATCCGTGATCTCGTGTGAGGAGGCCACTGGC 1802
 Db 18 CCTGCTGGAGGGCCCTGAGGGCTTGTGAGCTGGGGCTGCT 77
 Qy 1803 AGTTACTGATAACCACCTCCGGATGACACCCAGTCTTGTGCTGGGAGTCCGCTC 1862

RESULT 7 AQ875053/C 859 bp DNA linear strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
 LOCUS V120F6 mTH-3XHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
 DEFINITION AQ875053
 ACCESSION AQ875053.1 GI:6287297
 KEYWORDS GSS.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 SOURCE Saccharomyctales; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 COMMENT 1 (bases 1 to 859)
 REFERENCE 1 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., deSetages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M.
 AUTHOR Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption (1999)
 JOURNAL Unpublished
 CONTACT Kumar A
 Michael Snyder, Dept. of Mol. Cell. and Dev. Biology

Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: anuj.kumar@yale.edu
 Seq primer: GGCCRCCGTTCTTGGAAAGTAC
 Class: transposon-tagged.
 Location/Qualifiers
 1..859
 /organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /strain="Y2278 - S288C background, cir(0) rho(0)"
 /db_xref="taxon:4932"
 /la5_host="E. coli"
 /clone_lib="mTn-3XHA/1lacZ Insertion Library, strain Y2278"
 /note="Vector: pHS6-Sal; A yeast genomic DNA library
 without 2 micron or mitochondrial DNA was prepared in
 pHS6-Sal; genomic DNA was size-fractionated (DNA of
 roughly 2-3 kb in length) prior to cloning. This library
 was subsequently mutagenized with a mTn-3XHA/lacZ
 mini-transposon containing lacZ, URA3, and tet resistance."
 FEATURES SOURCE

Qy 1484 CAACCAACATTGGTTCTT 1502
 Db 142 AGACCAACATTCCCTCCT 124
 RESULT 8
 LOCUS BF251052
 DEFINITION EST418309 Coccidioides immitis spherule cDNA library Coccidioides immitis CDNA clone CIAAB85 5' sequence, mRNA sequence.
 ACCESSION BF251052
 VERSION BF251052.1 GI:16931195
 KEYWORDS EST.
 ORGANISM Coccidioides immitis
 SOURCE Coccidioides immitis
 REFERENCE Gardner, M.J. and Kirkland, T.
 AUTHORS Generation of ESTs from Coccidioides immitis spherule cDNA library
 TITLE Unpublished (2000)
 JOURNAL Contact: Malcolm J. Gardner
 COMMENT Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org
 FEATURES SOURCE
 1..637
 /organism="Coccidioides immitis"
 /mol_type="mRNA"
 /db_xref="taxon:5501"
 /clone="CIAAB85"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /clone_lib="Coccidioides immitis spherule cDNA library"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XbaI"
 ORIGIN

Query Match 6.2%; Score 223.4; DB 28; Length 859;
 Best Local Similarity 59.9%; Pred. No. 4.5e-41;
 Matches 407; Conservative 0; Mismatches 268; Indels 4; Gaps 2;
 Features Source
 Qy 827 AACGTGCTGTGATTAACCCCTCAGGATAATTGAAGTGCAGATCCTGGGATCACACTGGAG 886
 Db 801 AAATTCCTGGACARGGAAAGCATATTGAAGTTCAATTGAACTTGATTTGTTGGCCGATAACACGAAA 742
 Qy 887 AAGTTGTAACACCTTTATGAAACGTGACTGCTCAACTGCGGGTCGTCAACCAAAGTTGTGC 946
 Db 741 CGTTGTTCATCTTTGAAAGAGACTGTTGGTGCAGAGAA-CACCAAAAGGTGTCA 683
 Qy 947 AAATTGGCCAGCACAGCAACTTGGATTCAGAAACTGCGTATTTGTGGGATGCG 1006
 Db 682 AAGTGGCNCCAGAAAGACTTACNCCTGAAAGTCGGTGAAGTCGGTGAACGATGCGCAAGATGCGAG 623
 ORIGIN
 Query Match 6.1%; Score 220.2; DB 10; Length 637;
 Best Local Similarity 60.4%; Pred. No. 2.2e-40;
 Matches 380; Conservative 0; Mismatches 248; Indels 1; Gaps 1;
 Features Source
 Qy 685 TACCCCATCTTGTGAAGGGCAGTTGCGCGGTGGTGGGACGGGTATGCCGTTTGTGCT 744
 Db 7 TTCCCCATCATCATCAAGGGCCCTTGGCGGGGTGGCCATGCGTGTGCTCCGC 66
 Qy 745 TCACCTGATGAGCTTGCACAAATTAGCAACAGAACATCTCGTGAAGCTGAAGGGTTTC 804
 Db 67 GACCAAGAGTCCTCCGGGAACCTCTGGAGGCCAAATCGCCTTC 126
 Query Match 6.1%; Score 220.2; DB 10; Length 637;
 Best Local Similarity 60.4%; Pred. No. 2.2e-40;
 Matches 380; Conservative 0; Mismatches 248; Indels 1; Gaps 1;
 Features Source
 Qy 622 TAATATTGGCCAAGAGTGTGGCTACAGAAATGCGGGTACTGCTGAATTCTGGTTGATA 563
 Db 562 ACCAAATAGACACTATTCAATTCAAAAGTGGAAACATACCATCA 503
 Qy 1067 AAAGGGCAACCAACGTCTCATCGAAATGAACCTCACGTATCCAGGTGAGGACACCGTGA 1126
 Db 502 CAGAAGAAATTACCGGTTATAGATATTGTGGGGCTCAAGATCCAATTGCGGCAAGTGGCT 443
 Qy 1127 CTGAAGAAAGTCACCGGAGGTGGACACTGGTGAAGGGCAGATGGCTGGTGGCAGA 1186
 Db 442 CCTAACCCAGCTGGCCATTCCAGGAAAGATCCAACAGGCTTCGGCCAGATACCGGAACCTCAGCTGCAGT 383
 Qy 1187 CCTTGAAGGAATTGGTGTGACCCAGAAAGATAAGATCAAGAACCTCAGCATATTGAAGTGGCAG 864
 Db 442 CCTAACCCAGCTGGCCATTCCAGGAAAGATCCAACAGGCTTCGGCCAGATACCGGAACCTCAGCTGCAGT 383
 Qy 1247 GCCGCATCACCGGAAGATCCAACAGGCTTCGGCCAGATACCGGAACCTCAGCTGCAGT 323
 Db 382 GCGGTATTACCGGAAGACCCCTGCTAAGAACCTCAACAGATAACGGTAGATAAGAG 323
 Qy 1307 CGTACCGCTTACCGGGAGCTGGCTTCGTTGACGGTGAAGTGGCTGGTCTGGT 1363
 Db 322 TGTACCGTCTGCAAGGGTAATGGTGTAAACTGGATGGTGTAAACGCCTATGGTCA 263
 Qy 1364 CGGAATCACCGCAACACTTGAATGGCTGGTGAAGAACCTGGCTGGTCTGGT 1423
 Db 262 CAATAATCTCACCTATTACGACTCAATGCTGTTCAATTGCTCATGGTCA 203
 Qy 1424 TTGAAACTGCTGTTGGCTGTGCAAGGGCGGTGGCTGAGTTACCCGTCTTCAATGGAAATGAACCCACGT 1104
 Db 202 ACGAATGTTGCTGAAAGAAATGATTGTGCTTAATCGAGTTCAAATTAGGGTGTCA 143
 Qy 985 GATCGCATTGGAAATTCTGGTGGATGCAAGTAAAGTGGCTCATGGGCGGGGA 1044
 Db 307 GACGGCATCCTGGCGAACGGTCCGTCAGCTGGTCAAGCTGGTCAACGGCTAACGGCTACGCTACGGTCAACCCCGGC 366
 Qy 1045 ACCGGGAAATTCTGGTGGATGCAAGTAAAGTGGCTCATGGGCGGGGA 1104
 Db 367 ACCGGGAGTTCTGGTGGTCAACGGCTACGCTACGGTCAACCCCGGC 426

FEATURES	Source	Query Match Score	Local Similarity	Best Matches	Conservative	Pred. No.	Mismatches	Indels	Gaps	Length	Score
ORIGIN		6.0%	56.7%	421	421	1.8e-39	0	319	3	862	216.6
FEATURES		Score	Local Similarity	Best Matches	Conservative	Pred. No.	Mismatches	Indels	Gaps	Length	Score
ORIGIN		961	54.9%	1105	ATCCAGGTGAGCACCGTGAAGTCAACGGGACTGGTGAAGGGCAG	1164	QY	961	1164	862	216.6
ORIGIN		961	54.9%	427	ATCCAGGTGAGCACCATCACCGAGGATCACGGCATCGACATGTCGCCAG	486	Db	140	140	862	216.6
ORIGIN		961	54.9%	1165	ATGCCTGGCTGGCTGAACCTTGAGGAATTGGGTCTGACCCAAGATAAGATCAAG	1224	QY	1021	1021	862	216.6
ORIGIN		961	54.9%	487	ATCCAGATGCCGCCAACCTCGAGCTCGGGCATCCAGGACCGATCTCC	546	Db	200	200	862	216.6
ORIGIN		961	54.9%	1225	ACCCACGGTGAGCACTGCGCATCACCAACGGGCTTCG	1283	QY	1081	1081	862	216.6
ORIGIN		961	54.9%	547	ACCAAGGGTTCCGATCCAGTGGCGATCACACCAGAAGATCCCACAAAGGGCTTCCA	606	Db	260	260	862	216.6
ORIGIN		961	54.9%	1284	CCCAGATACCGGAACATATCACCGCGTACCG	1312	QY	1141	1141	862	216.6
ORIGIN		961	54.9%	607	GCCCCGACACCCGGTAAGATCGGAGGTCTACC	635	Db	320	320	862	216.6
RESULT	9			CA793824	862 bp mRNA linear EST 04-DEC-2002		QY	1201	1201	862	216.6
LOCUS	CA793824			AGENCOURT 11043532 NICHD XGC Emb1 Xenopus laevis cDNA clone IMAGE: 6865891 5', mRNA sequence.			Db	380	380	862	216.6
DEFINITION	CA793824			EST.			QY	1261	1261	862	216.6
ACCESSION	CA793824.1			GI:26042921 SOURCE Xenopus laevis (African clawed frog)			Db	440	440	862	216.6
VERSION	CA793824.1			Xenopus laevis; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopoda; Xenopus; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.			QY	1321	1321	862	216.6
KEYWORDS				(bases 1 to 862) NCI-CGAP http://www.ncbi.nlm.nih.gov/cnicgap.			Db	500	500	862	216.6
ORGANISM				National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)			QY	1378	1378	862	216.6
REFERENCE				Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. SOURCE Xenopus Preparation: Life Technologies, Inc. CDDNA Library Arrayed by: The I.M.A.G.E. Consortium (LInN) DNA Sequencing by: Agencourt Bioscience Corporation			Db	620	620	862	216.6
AUTHORS				Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1438	1438	862	216.6
TITLE				High quality sequence stop: 649. Location/Qualifiers			Db	620	620	862	216.6
JOURNAL				1.: /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="IMAGE:6865891" /tissue_type="embryo (stage 10)" /lab_host="DH10B (phage-resistant)" /clone_lib="NICHID XGC Emb1" /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."			QY	1498	1498	862	216.6
COMMENT				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	680	680	862	216.6
				High quality sequence stop: 649. Location/Qualifiers			QY	1558	1558	862	216.6
				1.: /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="IMAGE:6865891" /tissue_type="embryo (stage 10)" /lab_host="DH10B (phage-resistant)" /clone_lib="NICHID XGC Emb1" /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				High quality sequence stop: 649. Location/Qualifiers			Db	740	740	862	216.6
FEATURES				1.: /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="IMAGE:6865891" /tissue_type="embryo (stage 10)" /lab_host="DH10B (phage-resistant)" /clone_lib="NICHID XGC Emb1" /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			Db	740	740	862	216.6
FEATURES				Cloning information can be found through the I.M.A.G.E. Consortium/LInN at: http://image.llnl.gov Plate: LLNL14488 row: P column: 18			QY	1610	1610	862	216.6
ORIGIN			</td								

/organism="Drosophila melanogaster"
 /mol_type="mRNA"
 /db_xref="7227"
 /clone="GH08678"
 /sex="male and female"
 /dev_stage="adult"
 /lab_host="DH5 - alpha"
 /clone_lib="GH Drosophila melanogaster head POT2"
 /note="Organ: head; Vector: POT2; Site 1: EcoRI; Site 2:
 XbaI; Sized fractionated cDNAs were directly ligated into
 POT2. Plasmid cDNA library."
ORIGIN
 Query Match 6.0%; Score 216.4; DB 9; Length 675;
 Best Local Similarity 58.9%; Pred. No. 1.8e-39;
 Matches 392; Conservative 0; Mismatches 271; Indels 3; Gaps 1;
 1719 ACTGCCACGGGTTCCCGTGACCCGCCTGAAGCAGCTTGGCCAGCCGGCTTGCTCGTGA 1778
 8 ACCACCGAAGGGACTCCGGAGGTCCCTGGTGGTGGAAAGGTCCGGCTTGCCAAAGGA 67
 1779 TCTCCGTGAGCAGGACGCACTGGCAGTTACTGATAACCACCTTCGGGATGCACACCAGTC 1838
 68 GGTGGGCAACCGTAAGGAACCTGCTACTCATGGACACCACCTTCGGGATGCCACCAGTC 127
 1839 TTTCGCTTGGGACCCCAGTCCGCTCATTCGCACCTGAAGGCCTTGCGGAGGGCCGTGGCAA 1898
 128 GCTGCTGGCCACCCGGTCCACGATCTGCTGAAGATCTCCCCCTACGTGACGGCA 187
 1899 GCTGACTCCTGAGCTTTGTCTCGCTGGAGGGCTGGGGCTGGGGGGGACCTAACGATGGGCGAT 1956
 188 CAAGTCAACAAACCTGTATTGCTGGAGAACTGGGGGAGCCACCTTGACGTGGGCGT 247
 1959 GCGGTTCTCTGGGATTCGGATCCGGCTGACGGGCTGACCCGAGCTGGGAGATGCCGAA 2018
 248 GCGCTTCTGTGACGAGTGGCCCTGGGAGGGAGATGGCAAGGGCATCCCGGAA 307
 2019 TGTAAACATTGAGATGCTGCTTGGGATAACCCGGCAAACACCCGGATAACCCCGTAGCCAGA 2078
 308 CATTCCCTTCAGATGCTGGGGGAGCCAAACGGGCAACGGGCTACACCGCTATCCGGGA 367
 2079 CTCCGTCCTGCGGGCTTGTGTTAAGGAAGGCTGCCAGGCTCGGGTGGACATCTTCCGCAT 2138
 368 CAACGTTGGCTACAAGTTCTGTTGAGCTGGCTGTGCAAGACGGGATGGACATCTTCAGGGT 427
 2139 CTTCGACGGCCTTAACGACGTTCTCCAGATGCTCCAGGAATCGACGGCAGTCCTGGAGAC 2198
 428 GTTCGACTCGCTCAACTACCTGGCCAAACCTGATCTGGGATCTGGACATGGACATCTTCAGGGT 487
 2199 CAACACCCGGTAGCCGGGCTATGGCTTATTCTGGTGAATGGCTTGTGATCCAAATGCA 2258
 488 GGGGGGGTGGT---GGAGGGCTGCCATCTCCTATAACGGAGACGTAGGGATGGCTAGGG 544
 545 CACCAAGTATGATCTGAAATACTACACTAACCTTGCCGATGGCTAGGGATCCAAAGGGC 544
 2259 AAAGCTCTACCCCTGGATTACTACCTAAAGATGGCAGGGAGATGGTCAAGTCTGGCGC 2318
 545 CACCAAGTATGATCTGAAATACTACACTAACCTTGCCGATGGCTAGGGATCCAAAGGGC 604
 2319 TCACATCTTGGCCTTAAAGGATAATGGCTGGCTGGCTGCCAGGCTGCGTAACCAAGCT 2378
 605 CCACGGTGTCTGGCTTAAAGGATAATGGCTGGCTGGCTAAAGCCGAATCCGGCTTCT 664
 2379 GGTCAAC 2384
 665 GATCAC 670

		ORIGIN
Db	491 GCTGACCCTAGTCGCACTAAATACTCACTGGAGTACTACATGGGCTTAGCTGAGAACTG 550	Query Match 5.9%; Score 213.2; DB 14; Length 800; Best Local Similarity 59.1%; Pred. No. 1.1e-38; Matches 401; Conservative 0; Mismatches 273; Indels 4; Gaps 2;
Qy	2305 GTCAAAGTCTGGCCTCACATCTGGCCATTAAAGGATATGGCTGGCTGCTGGCCAGCT 2364	Qy 841 AACCTCAGGCATATTGAGTGCAG-ATCCTTGGGATCACACTGGAGAAGTTGACACCT 89.9
Db	551 GTGGGAGGTGGCACTCACATCCTGTGCAATTAGGACATGGGGCTGTGAAGGCC 610	Db 35 AAGCCACGGCACATCGAGTGGACATCTGGGACCTATGGGAACTCCCTGCACCT 94
Qy	2365 GCGGTAACCAAGCTGGTACCGCAACTGCGATCTGGCAGTGACGGT 2421	Qy 900 TTATGAACTGTGACTGCTCACTGCAGGTCAAGCTGGT 2481
Db	611 GCCTGCACATGCTGTCACTGGGACCTCCACTGCACATC 670	Db 95 GTACGAGGAGACTGCTCATCCAGGGCAACAGGTCGAGTGGCCATGCTGGCTGTGCAGCAGGG 154
Qy	2422 CACACCCACGACACTGGGAAACCTACTTGTGCAAGCTGGT 2495	Qy 960 ACAGCATTGGATCCAGAACTGCGTATGGGATGCGATAAGTTGTGCCG 1019
Db	671 CATACCCATGATAATCAGGGCAAGGTGTGGCAGCCATGCTGGCTGTGCAGCAGGG 730	Db 155 CGCCCACCTGGACCTGGACTCGGCTACCCAGGACTCTGTAAACTGGCTAA 214
Qy	2482 GCAGATGCTGTTGA 2495	Qy 1020 CTCCATTGGTTACAGGGGGAAACCGTGGATTCTTGGTGGATGAAAAGGGCAACCA 1079
Db	731 GCTGATGTCGTGGA 744	Db 215 ACAGGTGGGCTACCGAAACGGAGGACCGGAGCTGGACAGGCC 274
RESULT 12		Qy 1080 CGTCTTCATCGAAATGAAACCGTATCCAGGTGAGCACACCGTGACTGAAGAAGTCAC 1139
LOCUS	CK000115 800 bp mRNA linear EST 26-NOV-2003	Db 275 CTACTTCATCGAGGTCAACTCCGGCTGCGAGTGGACAGGGACAGGAGATCAC 334
DEFINITION	AGENCOURT 16368972 NIH MGC 220 Homo sapiens cDNA clone IMAGE : 30707731 5', mRNA sequence.	Qy 1140 CGAGGTGACCCAGATAAGATCAAGAACCCAGGATGGCAGTGGCTGCAACTTGAAGGAATT 1199
ACCESSION	CK000115	Db 335 CGACGTAGACCTGGTCCATGTCAGATCCACGGAGAACATCCGGCATCAACGGTCAACAGGGACAGGAGATCAC 454
VERSION	CK000115.1 GI:38526149	Qy 1200 GGGTCTGACCCAGATAAGATCAAGAACCCAGGATGGCAGTGGCTGCAACTTGAAGGAATT 1259
KEYWORDS	Homo sapiens (human)	Db 455 CGAGGACCCGGCGAGCTCCAGGGACACCGGGACATCCGGTCAACAGGGTCAACAGGGACAGGAGATCAC 514
ORGANISM	Homo sapiens	Qy 1260 GGAAAGTCCAAACAACAGGGTTCCGCCAGATAACGGAAACTATCACCGGTACCGCTCACC 1319
COMMENT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 80)	Db 515 AGAGGGCATGGGATATGCTTCGCTGGATAATGCTTCGCTCAAGGAGCCGTATCTCGCC 574
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/	Qy 1377 ACACTTGACTCCATGCTGGTAAATGACCTGGCTCGACTTTGAAACTGCTGT 1436
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Db 575 CCACTACGACTCCCTGCTCAAGTCATTGCCACGGGACACCCACGGCCGC 634
TITLE	Contact: Daniela S. Gerhard, Ph.D.	Qy 1437 TGCTCGGCACAGGGCGCTGAGTTCACGGTGTGGCTGGTGGAAACAACTTGG 1496
JOURNAL	Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov	Db 635 CACCAAGATGAGGGCCCTTGGGAGTTCCGGTCCAGGACCAACCATCGCG 694
KEYWORDS	Tissue Procurement: James Martin, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov	Qy 1497 TTTCTGGCAGGGCGCTGGTTGCT 1514
COMMENT	Plate: NDAM1072 row: m column: 20 High quality sequence start: 12 High quality sequence stop: 654.	Db 695 CTTCTGGCAAGATGTGCT 712
FEATURES	Location/Qualifiers 1. .800 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30707731" /lab_host="DH10B Tona" /clone_lib="NIH MGC 220" /note="Organ: mixed; Vector: PYX-ASC; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into PYX-ABC vector. Average insert size 0.5-1kb. Adaptors 5' (ATTGGGACGGAGG) 3' and 5' d (CCGGCCGGTGGAGAGGCC T18. Sequencing primers 3' end: T3 promoter primer 5' d (ATTAACCCCTCACTAAGGG) 3'. 5' End: T7 promoter primer 5' d (TAATACGACTACTATAGGG) 3'. Library was constructed in the laboratory of M. Bento Soares. Average insert size 3-4kb Note: this is a NIH_MGC Library."	RESULT 13 BI618593 LOCUS BI618593 mRNA linear EST 07-SEP-2001 DEFINITION RH49459.5prime RH Drosophila melanogaster normalized Head pFLIC-1 Drosophila melanogaster cDNA clone RH49459 5 similar to BCDNA:GH06348: FBan001516 GO:[pyruvate carboxylase (GO:0004736)] Located on: 2R 46B14-46C1; 08/19/2001, mRNA sequence. ACCESSION BI618593 VERSION BI618593.1 KEYWORDS EST. SOURCE Drosophila melanogaster (fruit fly) ORGANISM Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila. REFERENCE 1 (bases 1 to 640) AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Farfan,D., Frise,E., Carlson,J., Champe,M., Dorsett,V., Chavez,C., Dorsett,V., Farfan,D., Frise,E., Carlson,J., Champe,M., Dorsett,V., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
Source		

George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.

TITLE BDGP/HMI RH Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic AB003831: arm:2R [4876906, 5137815]
estimated-cyto:46B13-46E4: 08/19/2001
Plate: RH.494 row: E column: 11
High quality sequence stop: 543.

FEATURES Source
Location/Qualifiers
1. 640
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RH49459"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha Tora"
/clone_lib="RH Drosophila melanogaster normalized Head
PFLC-1"
/note="Organ: head; Vector: pFL1; Site 1: XbaI; Site 2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
ORIGIN

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
790	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
791	1		ORGIN
792	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
793	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
794	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
795	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
796	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
797	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
798	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
799	1		ORGIN
800	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
801	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
802	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
803	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
804	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
805	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
806	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
807	1		ORGIN
808	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
809	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
810	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
811	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
812	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
813	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
814	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
815	1		ORGIN
816	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
817	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
818	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
819	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
820	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
821	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
822	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
823	1		ORGIN
824	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
825	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
826	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
827	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
828	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
829	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
830	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
831	1		ORGIN
832	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
833	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
834	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
835	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
836	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
837	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Query Match 5.8%; Score 211; DB 12; Length 640;
Best Local Similarity 59.4%; Pred. No. 3.2e-38;
Matches 377; Conservative 0; Mismatches 255; Indels 3; Gaps 1;

Qy	Db	Features	Source
838	1		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493803" /tissue_type="anaplastic oligodendrogloma with LP/19q loss" /lab_host="DH110B (T1 phage-resistant)" /clone_lib="NCI CGAP_Brn67" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."
839	1		ORGIN
840	1		Query Match 5.7%; Score 208.2; DB 12; Length 715; Best Local Similarity 56.8%; Pred. No. 1.5e-37; Matches 403; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
841	1		Qy 872 GCGATCACCTGGAAAGTTGACACCTTTATGAACGTGACTGCCTCACTGCAGCGTCGTC 931 Db 1 GGGACCAGTATGGAAACATCCCTGCACCTGTACGGGGAGACTGCTCCATCCAGGGCGGC 60
842	1		Qy 932 ACCAAAAGTTGTCGAATTGGCATTTGGATCCAGAACGGCATTTGGATCCAGAACTGGGTGATCGCA 991 Db 61 ACCGAAGGTGGTCGAGATTGCCCGCCACCTGGGACTCTGGAAACGGCAACGGTGG 1051
843	1		Qy 992 TTGTCGGGATGCGATAAGTTGCTCCATTGGTTACAGGGGGAAACCGTGG 1111 Db 121 TCACCAAGGACTCTGTGAACAGGTGGCTACGGACCCGGCT 180
844	1		Qy 1052 ATTCTTGGTGGATGAAACAGCTTCACTGAATGAACCCACGTATCCAGG 240 Db 181 AGTRCCCTGGTGGACAGGGCAAGGACTACTTCATCGAGGCTCCCTGCAGG 240
845	1		Qy 1112 TTGAGCACACCGTGAAGAAGTCACCGAGGTGGACCTGGTGAAGGGCAGATGGCCT 1171 Db Qy

Best Local Similarity 58.9%; Pred. No. 1.1e-36; Matches 371; Conservative 0; Mismatches 256; Indels 3; Gaps 1;					
Db	241	TGGAGCACACGGTCACAGGAGATCACCGAACCTAGACCTGGTCCATGCTCAGATCCACG	300		
Qy	1172	TGGCTGGTGAACCTTGAAAGGAATTGGGTCTGACCCAAGATAAGATCAAGACCCACG	1231		
Db	301	TGGCTAGGGCAGGCCAACCTGGGACCTGGGAGGAAACATCGCATCAACG	360		
Qy	1232	GTCAGGCACTGCAGTGGCCATCACCCAGGAAAGATCCACCAACGGCTTCGCCAGATA	1291		
Db	361	GGTGTGCCATCCAGTGGGTCAACCACCGGAGGACCCGGGATGGGACAGAGAAGGACAGACA	420		
Qy	1292	CCGGAACATCACCGCTACCGGAGGCTGGGTTGGCTGACGGGTGAG	1351		
Db	421	CGGGCGCATTGAGGTGTTCGGGAGGGCATGGGATCGGCTGGATAATGCTT	480		
Qy	1352	CTCAGCTC--GGTGGGMAATCACCGCACACTTGACTCCATGCTGGAAATGACCT	1408		
Qy	1409	GCGGTGGTTCCGACTTTGAAACTGGCTGGCAACAGCGGACACCGTGAAGTTCAC	1468		
Db	541	CCGCCTTCCAAGGAGGCCATCTGCCCAACTACGACTCCCTGCTGGTCAAAGTCATTG	540		
Qy	1469	CCGTTGGTCTGGTCAACATGGCTGGCTGGCAACAGCGGAGGACT	1528		
Db	601	GGTTCGAGGTGTGAAGGACCAACCGGCCAACAAAGGAGGAAACAGGAGCT	660		
Qy	1529	TCACTTCCAAGGGCATCGCCACCGGATTCATGCCGATCACCCGCACCT	1577		
Db	661	TCCTGGCAGGGCACTGTGGACACCAACTCATCGACGGAGGAAACCCAGAGCT	709		
RESULT	15				
LOCUS	BJ063722	641 bp mRNA linear EST 29-SEP-2003			
DEFINITION	BJ063722 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL077c10 5', mRNA sequence.				
ACCESSION	BJ063722				
VERSION	BJ063722.1	GI:17470882			
KEYWORDS	EST.	CACTTTGACTCCATGGTGGATTGAGTTGGCTGGTCTGGTCAAGCTGGTGT	1437		
SOURCE	Xenopus laevis (African clawed frog)				
ORGANISM	Xenopus laevis				
REFERENCE	AUTHORS	Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.			
JOURNAL		Expressed genes in X. laevis embryo			
COMMENT		Unpublished (2001)			
	Contact: Tadasu Shin-i				
	Center For Genetic Resource Information				
	National Institute of Genetics				
	1111 Yata, Mishima, Shizuoka 411-8540, Japan				
	Tel: 81-559-81-6856				
	Fax: 81-559-81-6855				
	Email: tshini@genes.nig.ac.jp				
FEATURES	Source	The information of this clone is available through the following URL.			
		http://xenopus.nibb.ac.jp/			
	Location/Qualifiers				
	1: .641				
	/organism="Xenopus laevis"				
	/mol_type="mRNA"				
	/db_xref="taxon:8355"				
	/clone="XL077c10"				
	/tissue_type="whole embryo"				
	/dev_stage="stage 25"				
	/clone_lib="NIBB Mochii normalized Xenopus tailbud library"				
	ORIGIN				